Mesodinium chamaeleon data analysis, revision 1

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Loading of packages and data

```r
# LOAD RELEVANT PACKAGES
require(Rmisc) #has summarySE function, which is quite useful
```

```
## Loading required package: Rmisc
```

```
## Loading required package: lattice
```

```
## Loading required package: plyr
```

```r
require(sciplot) #has bargraph.CI function
```

```
## Loading required package: sciplot
```

```r
require(pracma)
```

```
## Loading required package: pracma
```

```r
# IMPORT DATA
#setwd("~/GoogleSync/KarmaChamaeleon/JPhyc_R1/RAnalysis") # set working directory
dat<-read.csv('Meso_TS.csv',header=TRUE) # Timeseries of M. chamaeleon data
crypto.dat <- read.csv('Crypto_TS.csv',header=TRUE) # Timeseries of cryptophyte data
growth<-read.csv('GrowthRates.csv',header=TRUE) # Growthrates file
pe <- read.csv('MC_PEcurveData.csv',header=TRUE) # M. chamaeleon photosynthesis-irradiance data
pe.crypto <- read.csv('Crypto_PEcurvedata.csv',header=TRUE) # Cryptophyte photosynthesis-irradiance dat
carbon <- read.csv('CHN.csv',header=TRUE) # CHN data

# Adjust necessary data into numeric form; create ID columns
#str(dat)
dat$ID <- paste(dat$Prey,dat$Light,dat$Fed,dat$Rep,sep='.')
dat$Pmax_chl <- dat$Pmax*0.06332817 # The multiplier 0.06332817 converts from electrons per chlorophyll
dat$Pmax_cell <- dat$Pmax_chl*as.numeric(as.character(dat$corr_chl_p_cell))
```

```
## Warning: NAs introduced by coercion
```

```r
dat$PI_chl <- dat$ETR_I*0.06332817
dat$PI_cell <- dat$PI_chl*as.numeric(as.character(dat$corr_chl_p_cell))
```

```
## Warning: NAs introduced by coercion
```

```r
dat$chl_p_cell <- as.numeric(as.character(dat$corr_chl_p_cell)) # Sometimes R incorrectly imports data
```

```
## Warning: NAs introduced by coercion
```

```r
dat$chl_p_mL <- dat$chl_p_cell*dat$MC_cellspmL/1000
dat$PlastidCount <- as.numeric(as.character(dat$PlastidCount))
```

```
## Warning: NAs introduced by coercion
```

```r
#str(crypto.dat)
crypto.dat$ID <- paste(crypto.dat$Prey,crypto.dat$Light,crypto.dat$Rep,sep='.')
crypto.dat$Pmax_chl <- crypto.dat$Pmax*0.06332817
```

```
crypto.dat$Pmax_cell <- crypto.dat$Pmax_chl*crypto.dat$ChlpCell
crypto.dat$PI_chl <- crypto.dat$P_I*0.06332817
crypto.dat$PI_cell <- crypto.dat$PI_chl*crypto.dat$ChlpCell

pe$ETR.C <- pe$ETR*0.06332817 # The multiplier 0.06332817 converts from electrons per chlorophyll molec


# SET PLOTTING PARAMETERS (COLOURS)
Acol <- 'red' # colour to plot rep A data
Bcol <- 'blue' # colour to plot rep B data
Ccol <- 'green' # colour to plot rep C data
Fedcol <- 'black'
Starvedcol <- 'gray80'
Cryptocol <- 'gray50'

SMcol <- 'firebrick'
RScol <- 'lightcoral'
CMcol <- 'seagreen'
HPcol <- 'turquoise3'
preycolvec <- c(CMcol,HPcol,RScol,SMcol)

days <- unique(dat$ExptDay)
```

Computations

Revision 1: Supplemental Figure: C per cell

```
head(carbon)
```

```
##    Species Prey Rep Light ngC_cell
## 1       MC   CM   A    10    0.954
## 2       MC   CM   B    10    0.963
## 3       MC   CM   C    10    1.080
## 4       MC   HP   A    10    0.480
## 5       MC   HP   B    10    0.670
## 6       MC   HP   C    10    0.651
```
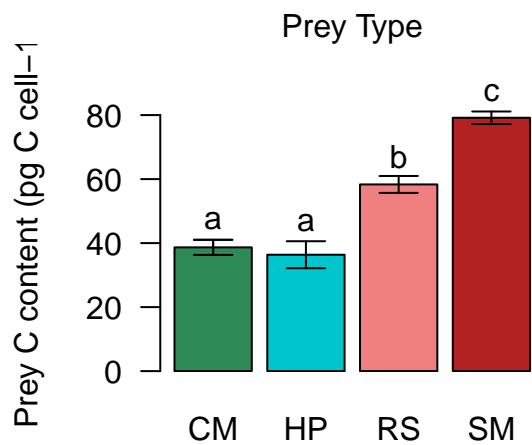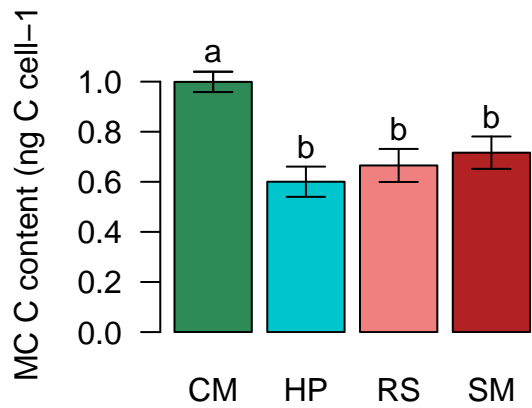
```
par(mar=c(4,4,1,1),mfrow=c(2,1))
bargraph.CI(Prey,ngC_cell,data=carbon[carbon$Species=='MC',],las=1,xlab='Prey Type',ylab='MC C content
# TukeyHSD(aov(ngC_cell~Prey,data=carbon[carbon$Species=='MC',]))

bargraph.CI(Species,ngC_cell*1000,data=carbon[carbon$Species!='MC',],las=1,xlab='Cryptophyte',ylab='Prey
```

```
#TukeyHSD(aov(ngC_cell~Species,data=carbon[carbon$Species!='MC',]))
```

Revision 1: Incorporating C per cell

```r
# M. chamaeleon
MC.C <- summarySE(data=carbon[carbon$Species=='MC',],measurevar='ngC_cell',groupvar='Prey')
dat$Cpercell <- MC.C$ngC_cell[match(dat$Prey,MC.C$Prey)]
dat$ChlperC <- dat$chl_p_cell/dat$Cpercell
dat$Pmax_C <- dat$Pmax_cell/dat$Cpercell
dat$PI_C <- dat$PI_cell/dat$Cpercell

# Cryptophytes
prey.C <- summarySE(data=carbon[carbon$Species!='MC',],measurevar='ngC_cell',groupvar='Species')
crypto.dat$Cpercell <- prey.C$ngC_cell[match(crypto.dat$Prey,prey.C$Species)]
crypto.dat$ChlperC <- crypto.dat$ChlpCell/crypto.dat$Cpercell
crypto.dat$Pmax_C <- crypto.dat$Pmax_cell/crypto.dat$Cpercell
crypto.dat$PI_C <- crypto.dat$PI_cell/crypto.dat$Cpercell
```

Computing maxima

```r
# Pick max crypto response

crypto.max <- as.data.frame(unique(crypto.dat$ID))
colnames(crypto.max) <- c('ID')
crypto.max$Prey <- crypto.dat$Prey[match(crypto.max$ID,crypto.dat$ID)]
crypto.max$Light <- crypto.dat$Light[match(crypto.max$ID,crypto.dat$ID)]
crypto.max$Rep <- crypto.dat$Rep[match(crypto.max$ID,crypto.dat$ID)]
crypto.max$chl <- NaN; crypto.max$FvFm <- NaN; crypto.max$P_I <- NaN; crypto.max$a <- NaN; crypto.max$Pr
# Revision 1:
crypto.max$PI_C <- NaN; crypto.max$Pmax_C <- NaN; crypto.max$ChlperC <- NaN

for(i in 1:length(unique(crypto.dat$ID))){
    hold <- crypto.dat[crypto.dat$ID==unique(crypto.dat$ID)[i],]
    crypto.max$chl[i] <- max(hold$ChlpCell,na.rm=TRUE)
    hold2 <- hold
    if(hold$Prey[1]=='CM'){ hold2 <- hold[hold$ExptDay%in%c(0,1),]}
    crypto.max$FvFm[i] <- max(hold2$Fv.Fm,na.rm=TRUE)
    hold <- hold[hold$ExptDay%in%c(0,1,2,4),]
    crypto.max$P_I[i] <- max(hold$P_I,na.rm=TRUE)
    crypto.max$Pmax[i] <- max(hold$Pmax,na.rm=TRUE)
    crypto.max$a[i] <- max(hold$a,na.rm=TRUE)
    crypto.max$Pmax_chl[i] <- max(hold$Pmax_chl,na.rm=TRUE)
    crypto.max$Pmax_cell[i] <- max(hold$Pmax_cell,na.rm=TRUE)
    crypto.max$PI_chl[i] <- max(hold$PI_chl,na.rm=TRUE)
    crypto.max$PI_cell[i] <- max(hold$PI_cell,na.rm=TRUE)
    # Revision 1:
    crypto.max$PI_C[i] <- max(hold$PI_C,na.rm=TRUE)
    crypto.max$Pmax_C[i] <- max(hold$Pmax_C,na.rm=TRUE)
    crypto.max$ChlperC[i] <- max(hold$ChlperC,na.rm=TRUE)
}

MC.max <- as.data.frame(unique(dat$ID))
colnames(MC.max) <- c('ID')
MC.max$Prey <- dat$Prey[match(MC.max$ID,dat$ID)]
MC.max$Light <- dat$Light[match(MC.max$ID,dat$ID)]
MC.max$Fed <- dat$Fed[match(MC.max$ID,dat$ID)]
MC.max$Rep <- dat$Rep[match(MC.max$ID,dat$ID)]
MC.max$chl <- NaN; MC.max$FvFm <- NaN; MC.max$P_I <- NaN; MC.max$a <- NaN; MC.max$Pmax <- NaN; MC.max$Pr
MC.max$plastids <- NaN

# Revision 1:
MC.max$ChlperC <- NaN; MC.max$Pmax_C <- NaN; MC.max$PI_C <- NaN

for(i in 1:length(unique(dat$ID))){
    hold <- dat[dat$ID==unique(dat$ID)[i],]
    hold <- hold[hold$ExptDay%in%c(0,1,2,4,6),]
    MC.max$P_I[i] <- max(hold$ETR_I,na.rm=TRUE)
    MC.max$a[i] <- max(hold$a,na.rm=TRUE)
    MC.max$Pmax[i] <- max(hold$Pmax,na.rm=TRUE)
    MC.max$Pmax_chl[i] <- max(hold$Pmax_chl,na.rm=TRUE)
    MC.max$Pmax_cell[i] <- max(hold$Pmax_cell,na.rm=TRUE)
```

```r
    MC.max$PI_chl[i] <- max(hold$PI_chl,na.rm=TRUE)
    MC.max$PI_cell[i] <- max(hold$PI_cell,na.rm=TRUE)
    hold <- hold[hold$ExptDay%in%c(0,1,2,4),]
    MC.max$chl[i] <- max(hold$chl_p_cell,na.rm=TRUE)
    MC.max$FvFm[i] <- max(hold$FvFm,na.rm=TRUE)
    MC.max$plastids[i] <- max(hold$PlastidCount,na.rm=TRUE)

    # Revision 1:
    MC.max$ChlperC[i] <- max(hold$ChlperC,na.rm=TRUE)
    MC.max$Pmax_C[i] <- max(hold$Pmax_C,na.rm=TRUE)
    MC.max$PI_C[i] <- max(hold$PI_C,na.rm=TRUE)
}

crypto.max$Prey.Light <- paste(crypto.max$Prey,crypto.max$Light,sep='.')
MC.max$Prey.Light <- paste(MC.max$Prey,MC.max$Light,sep='.')
MC.max$Treat.Rep <- paste('1802',MC.max$ID,sep='.')

MC.max$relFvFm <- NaN
MC.max$relP_I <- NaN
MC.max$rela <- NaN
MC.max$relPmax <- NaN
MC.max$relPmax_chl <- NaN
MC.max$relPI_chl <- NaN

# Revision 1:
MC.max$relPI_C <- NaN
MC.max$relPmax_C <- NaN


for(i in 1:dim(MC.max)[1]){
    # Compute relative MC FvFm
    callID <- MC.max$Prey.Light[i]
    MC.max$relFvFm[i] <- MC.max$FvFm[i]/mean(crypto.max[crypto.max$Prey.Light==callID,]$FvFm,na.rm=TRUE)

    # Compute relative MC P_I
    MC.max$relP_I[i] <- MC.max$P_I[i]/mean(crypto.max[crypto.max$Prey.Light==callID,]$P_I,na.rm=TRUE)

    # Compute relative MC a
    MC.max$rela[i] <- MC.max$a[i]/mean(crypto.max[crypto.max$Prey.Light==callID,]$a,na.rm=TRUE)

    # Compute relative MC P_max
    MC.max$relPmax[i] <- MC.max$Pmax[i]/mean(crypto.max[crypto.max$Prey.Light==callID,]$Pmax,na.rm=TRUE)

    # Compute relative MC P_max per chl
    MC.max$relPmax_chl[i] <- MC.max$Pmax_chl[i]/mean(crypto.max[crypto.max$Prey.Light==callID,]$Pmax_chl

    # Compute relative MC P_I per chl
    MC.max$relPI_chl[i] <- MC.max$PI_chl[i]/mean(crypto.max[crypto.max$Prey.Light==callID,]$PI_chl,na.r

    # Revision 1:
    # Compute relative MC P_I per C
    MC.max$relPI_C[i] <- MC.max$PI_C[i]/mean(crypto.max[crypto.max$Prey.Light==callID,]$PI_C,na.rm=TRUE
    # Compute relative MC P_max per C
```

```r
        MC.max$relPmax_C[i] <- MC.max$Pmax_C[i]/mean(crypto.max[crypto.max$Prey.Light==callID,]$Pmax_C,na.rm

    }

dat$Treat.Rep <- paste(dat$MCstrain,dat$Prey,dat$Light,dat$Fed,dat$Rep,sep='.')
#treat.data <- as.data.frame(unique(dat$Treatment))
growth$Treat.Rep <- paste(growth$MCstrain,growth$Prey,growth$Light,growth$Fed,growth$Rep,sep='.')

growth$ic <- NaN
growth$preyic <- NaN
growth$max <- NaN
growth$relincrease <- NaN
growth$relincreaseperprey <- NaN
for(i in 1:dim(growth)[1]){
    dat.hold <- dat[dat$Treat.Rep==growth$Treat.Rep[i],]
    growth$ic[i] <- dat.hold[dat.hold$ExptDay==0,]$MC_cellspmL
    growth$preyic[i] <- dat.hold[dat.hold$ExptDay==0,]$Prey_cellspmL
    growth$max[i] <- max(dat.hold$MC_cellspmL,na.rm=TRUE)
    growth$relincrease[i] <- growth$max[i]/growth$ic[i]
    growth$relincreaseperprey[i] <- (growth$max[i]-growth$ic[i])/growth$preyic[i]

}



growth$deltarelincreasefed <- NaN
for(i in 1:dim(growth[growth$Fed=='Y',])[1]){
  growth[growth$Fed=='Y',]$deltarelincreasefed[i] <- growth[growth$Fed=='Y',]$relincrease[i]-growth[grow
}




growth$TotPreyCons <- rep(0,dim(growth)[1])
times <- c(0,1,2,4,6,8,10,12,14)

for(i in 1:length(unique(dat$Treat.Rep))){
    callID <- unique(dat$Treat.Rep)[i]  # Select the dataset of interest
    if(growth[growth$Treat.Rep==callID,]$Fed=='Y'){ # If this is a fed dataset
        hold <- dat[dat$Treat.Rep==callID,]
        hold <- hold[!is.na(hold$MC_cellspmL),]
        prey <- hold$Prey_cellspmL
        MC <- hold$MC_cellspmL
        MC_init <- MC[1]
        graz <- growth[growth$Treat.Rep==callID,]$g
        fcn <- graz*prey
        for(j in 1:length(hold)[1]){if(is.nan(fcn[j])){fcn[j]<-0}}
        growth[growth$Treat.Rep==callID,]$TotPreyCons <- trapz(hold$ExptDay,fcn)
        growth[growth$Treat.Rep==callID,]$MC_init <- MC_init
    }
}

growth$PreyperMC <- growth$TotPreyCons/growth$ic
```

```r
# photosynthesis contributions

growth$chl.loss.rate <- NaN
growth$plastid.loss.rate <- NaN
growth$FvFm.decline <- NaN
growth$chl.decline <- NaN
growth$FvFm.pctdecline <- NaN
growth$chl.pctdecline <- NaN
growth$PI.perchl <- NaN
growth$Cfixforchl <- NaN
growth$chl.res.time <- NaN
growth$C.perchl <- NaN
growth$C.perprey <- NaN
growth$C.fromprey <- NaN
growth$C.fixed <- NaN
growth$C.fixed2 <- NaN

# Revision 1:
growth$Pmax.change <- NaN
growth$a.change <- NaN
growth$Pmax.pctchange <- NaN
growth$a.pctchange <- NaN

IDs <- unique(growth$Treat.Rep)
times <- c(0,1,2,4,6,8,10,12,14)
tsteps <- 5 # number of timesteps to use

for(i in 1:length(IDs)){
    # Choose the dataset
    callID <- IDs[i]
    hold <- dat[dat$Treat.Rep==callID,]

    # Determine rate of chlorophyll loss over first week
    chls <- log(hold$chl_p_cell)
    lm1 <- lm(chls[1:tsteps]~times[1:tsteps])
    if(hold$Prey[1]=="CM"){    lm1 <- lm(chls[2:tsteps]~times[2:tsteps])
    if(hold$Light[1]==10&hold$Rep[1]=='B'){ lm1 <- lm(chls[1:4]~times[1:4])    }}

    growth[growth$Treat.Rep==callID,]$chl.loss.rate <- summary(lm1)$coefficients[2,1]

    # Determine rate of plastid loss over first 48 hrs
    plastids <- log(hold$PlastidCount)
    lm2 <- lm(plastids[1:3]~times[1:3])
    growth[growth$Treat.Rep==callID,]$plastid.loss.rate <- summary(lm2)$coefficients[2,1]

    # Determine overall decline in Fv/Fm
    FvFm.init <- hold$FvFm[1]
    FvFm.min <- min(hold$FvFm,na.rm=TRUE)
    growth[growth$Treat.Rep==callID,]$FvFm.decline <- FvFm.init-FvFm.min
    growth[growth$Treat.Rep==callID,]$FvFm.pctdecline <- (FvFm.init-FvFm.min)/FvFm.init

    # Determine overall change in alpha
    a.init <- hold$a[1]
```

```r
    a.end <- hold$a[dim(hold)[1]]
    if(hold$Prey[1]=="CM"){if(hold$Light[1]==100){a.end <- hold$a[dim(hold)[1]-1]}} # Using Day 12 data
    growth[growth$Treat.Rep==callID,]$a.change <- a.init-a.end
    growth[growth$Treat.Rep==callID,]$a.pctchange <- (a.init-a.end)/a.init

    # Determine overall change in Pmax
    p.init <- hold$Pmax[1]
    p.end <- hold$Pmax[dim(hold)[1]]
    if(hold$Prey[1]=="CM"){if(hold$Light[1]==100){p.end <- hold$Pmax[dim(hold)[1]-1]}} # Using Day 12 da
    growth[growth$Treat.Rep==callID,]$Pmax.change <- p.init-p.end
    growth[growth$Treat.Rep==callID,]$Pmax.pctchange <- (p.init-p.end)/p.init

    # Determine overall decline in chl-a
    chla.init <- hold$chl_p_cell[1]
    chla.min <- min(hold$chl_p_cell,na.rm=TRUE)
    growth[growth$Treat.Rep==callID,]$chl.decline <- chla.init-chla.min
    growth[growth$Treat.Rep==callID,]$chl.pctdecline <- (chla.init-chla.min)/chla.init

    # Chlorophyll residence time
    growth[growth$Treat.Rep==callID,]$chl.res.time = -1/(growth[growth$Treat.Rep==callID,]$chl.loss.rat

    # Carbon fixed during that residence time
    PIs <- hold$PI_chl
    PI.mean <- mean(PIs[1:tsteps],na.rm=TRUE)
    growth[growth$Treat.Rep==callID,]$PI.perchl <- PI.mean
    growth[growth$Treat.Rep==callID,]$C.perchl <- PI.mean*growth[growth$Treat.Rep==callID,]$chl.res.tim

    # Carbon fixed per prey cell
    preychl <- mean(crypto.max[crypto.max$Prey==hold$Prey[1]&crypto.max$Light==hold$Light[1],]$chl,na.r
    growth[growth$Treat.Rep==callID,]$C.perprey <- preychl*growth[growth$Treat.Rep==callID,]$C.perchl

    # Carbon fixed from all prey across the experiment
    preycons <- mean(growth[growth$Fed=='Y'&growth$Prey==hold$Prey[1]&growth$Light==hold$Light[1],]$Pre
    growth[growth$Treat.Rep==callID,]$C.fromprey <- preycons*growth[growth$Treat.Rep==callID,]$C.perpre

    # Carbon fixed, calculated as integral of chl-a/cell * PI_chl
    hold <- hold[!is.na(hold$PI_cell),]
    growth[growth$Treat.Rep==callID,]$C.fixed <- trapz(hold$ExptDay,hold$chl_p_cell*hold$PI_chl*12) # m

    # Carbon fixed, calculated as integral of chl-a/mL * PI_chl divided by initial cells
    hold <- hold[!is.na(hold$chl_p_mL),]
    growth[growth$Treat.Rep==callID,]$C.fixed2 <- trapz(hold$ExptDay,hold$PI_chl*12*hold$chl_p_mL)/hold

}

growth$deltaCfixed <- NaN
for(i in 1:dim(growth[growth$Fed=='Y',])[1]){
  growth[growth$Fed=='Y',]$deltaCfixed[i] <- growth[growth$Fed=='Y',]$C.fixed2[i]-growth[growth$Fed=='N
}
```

Visualizing Data

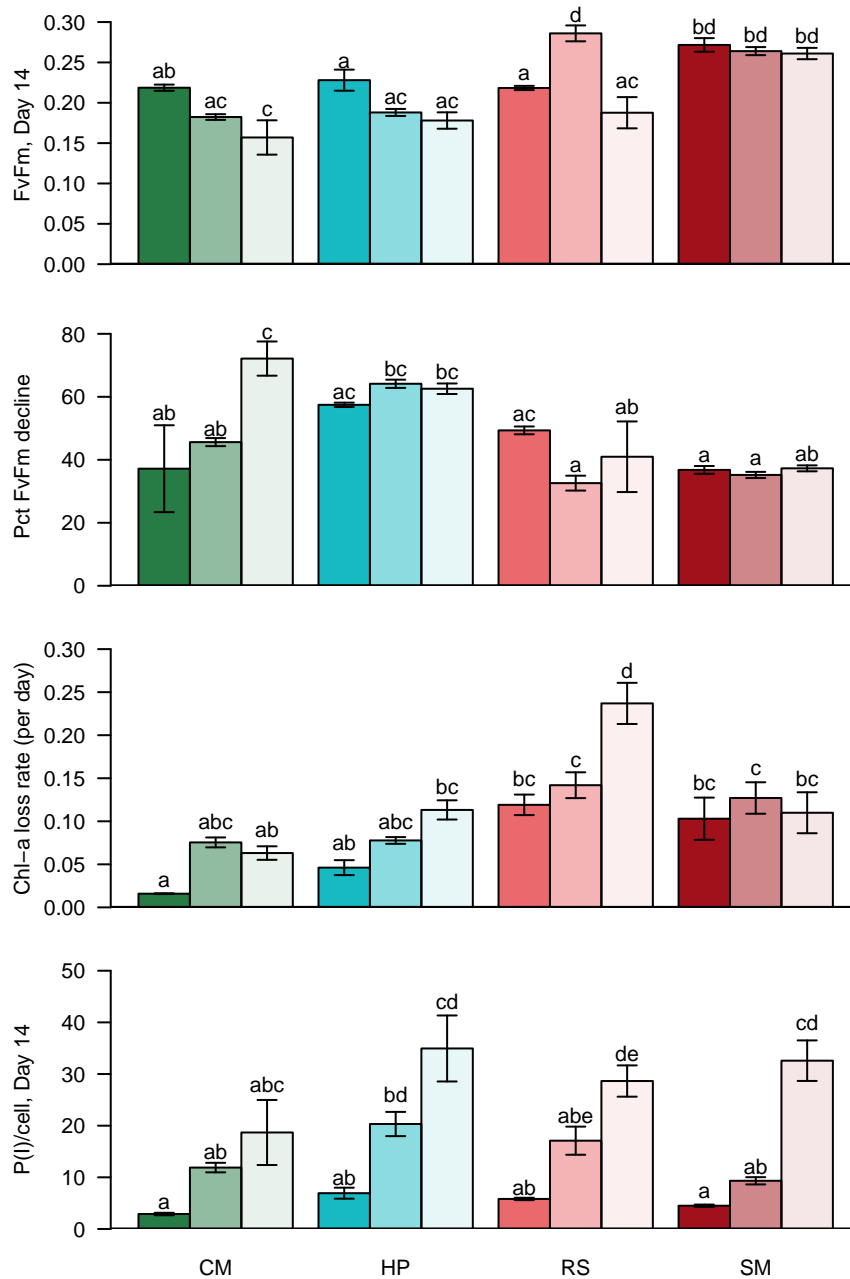**Figure 1: Loss of photosynthetic capacity in starved cultures**

```r
par(mar=c(2,4,0.5,0.5),mfrow=c(4,1))
xcoords <- c(1,2,3,4.5,5.5,6.5,8,9,10,11.5,12.5,13.5)

# FvFm at day 14
bargraph.CI(Prey,FvFm,group=Light,data=dat[dat$Fed=='N'&dat$ExptDay==14,],legend=FALSE,err.width=0.05,la
#TukeyHSD(aov(FvFm~Prey*as.factor(Light),data=dat[dat$Fed=='N'&dat$ExptDay==14,]))

# decline in FvFm
#bargraph.CI(Prey,FvFm.decline,group=Light,data=growth[growth$Fed=='N',],legend=FALSE,err.width=0.05,la
bargraph.CI(Prey,100*FvFm.pctdecline,group=Light,data=growth[growth$Fed=='N',],legend=FALSE,err.width=0
#TukeyHSD(aov(FvFm.pctdecline~Prey*as.factor(Light),data=growth[growth$Fed=='N',]))

# pigment decay rate
bargraph.CI(Prey,-1*(chl.loss.rate),group=Light,data=growth[growth$Fed=='N',],legend=FALSE,err.width=0.
#TukeyHSD(aov(-1*(chl.loss.rate)~Prey*as.factor(Light),data=growth[growth$Fed=='N',]))

# P(I) at day 14
bargraph.CI(Prey,PI_cell,group=Light,data=dat[dat$Fed=='N'&dat$ExptDay==14,],legend=FALSE,err.width=0.05
```

Figure 1, revision 1: Loss of photosynthetic capacity in starved cultures

```
par(mar=c(2,4,0.3,0.5),mfrow=c(3,2))
xcoords <- c(1,2,3,4.5,5.5,6.5,8,9,10,11.5,12.5,13.5)

# FvFm at day 14
bargraph.CI(Prey,FvFm,group=Light,data=dat[dat$Fed=='N'&dat$ExptDay==14,],legend=FALSE,err.width=0.05,la
#TukeyHSD(aov(FvFm~Prey*as.factor(Light),data=dat[dat$Fed=='N'&dat$ExptDay==14,]))
```

```r
# P(I) at day 14
bargraph.CI(Prey,PI_chl,group=Light,data=dat[dat$Fed=='N'&dat$ExptDay==14,],legend=FALSE,err.width=0.05
#TukeyHSD(aov(PI_chl~as.factor(Light)*Prey,data=dat[dat$Fed=='N'&dat$ExptDay==14,]))


# decline in FvFm
#bargraph.CI(Prey,FvFm.decline,group=Light,data=growth[growth$Fed=='N',],legend=FALSE,err.width=0.05,la
bargraph.CI(Prey,100*FvFm.pctdecline,group=Light,data=growth[growth$Fed=='N',],legend=FALSE,err.width=0
#TukeyHSD(aov(FvFm.pctdecline~Prey*as.factor(Light),data=growth[growth$Fed=='N',]))

# pigment decay rate
bargraph.CI(Prey,-1*(chl.loss.rate),group=Light,data=growth[growth$Fed=='N',],legend=FALSE,err.width=0.0
#TukeyHSD(aov(-1*(chl.loss.rate)~Prey*as.factor(Light),data=growth[growth$Fed=='N',]))


# Revision 1:
# pct change in alpha
# bargraph.CI(Prey,-100*a.pctchange,group=Light,data=growth[growth$Fed=='N',],legend=FALSE,err.width=0.

# pct change in Pmax
# bargraph.CI(Prey,-100*Pmax.pctchange,group=Light,data=growth[growth$Fed=='N',],legend=FALSE,err.width

# change in alpha
bargraph.CI(Prey,-a.change,group=Light,data=growth[growth$Fed=='N',],legend=FALSE,err.width=0.05,las=3,
#TukeyHSD(aov(a.change~as.factor(Light)*Prey,data=growth[growth$Fed=='N',]))

# change in Pmax
bargraph.CI(Prey,-Pmax.change,group=Light,data=growth[growth$Fed=='N',],legend=FALSE,err.width=0.05,las=
```
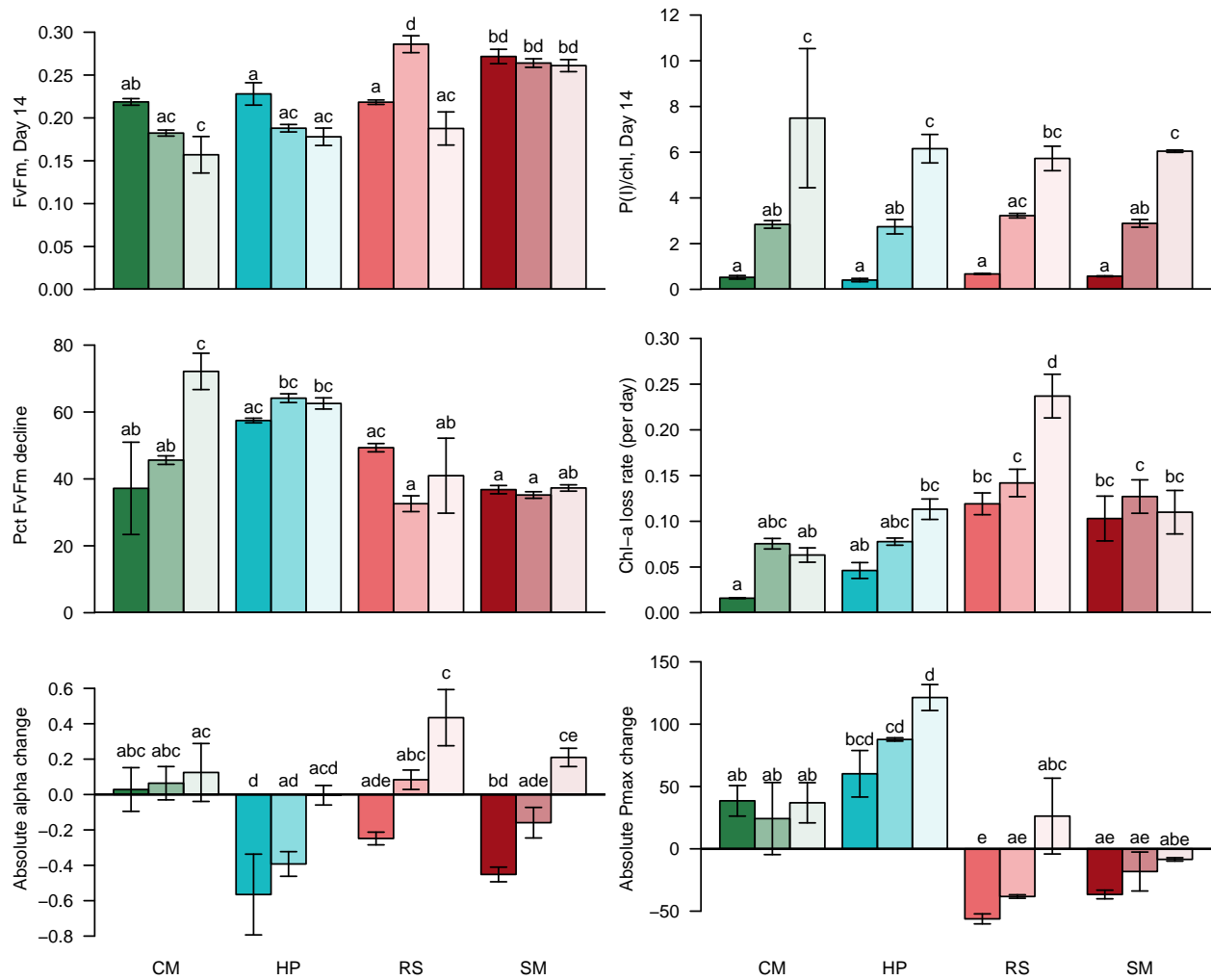
```
#TukeyHSD(aov(Pmax.change~as.factor(Light)*Prey,data=growth[growth$Fed=='N',]))
```

Supplementary Figure: PE curves over time, by prey and light level, measured in electron transport per chlorophyll-a

```
# Note: this is in electron transport rate (electrons per s per chl-a)
# To convert to C, multiply by *0.06332817


pe.summ <- summarySE(data=pe,'ETR',groupvars=c('Prey','Light','Fed','ExptDay','PAR'),na.rm=TRUE)


preychoice_set <- c('CM','HP','RS','SM')
lightchoice_set <- c(10,50,100)
ymax_set <- c(100,130,200)

days <- unique(pe.summ$ExptDay)
bgvec <- rev(c('gray90','gray80','gray70','gray60','gray50','gray40','gray30','gray20','black'))
```

```r
par(mar=c(1,1,0.5,0.5))
layout(matrix(c(rep(c(13,1,1,1,2,2,2,3,3,3,4,4,4),3),rep(c(13,5,5,5,6,6,6,7,7,7,8,8,8),3),rep(c(13,9,9,9
```

```
## Warning in matrix(c(rep(c(13, 1, 1, 1, 2, 2, 2, 3, 3, 3, 4, 4, 4), 3),
## rep(c(13, : data length [133] is not a sub-multiple or multiple of the
## number of rows [10]
```

```r
for(lightctr in 1:length(lightchoice_set)){
    lightchoice <- lightchoice_set[lightctr]
    ymaxchoice <- ymax_set[lightctr]

for(preyctr in 1:length(preychoice_set)){
  preychoice = preychoice_set[preyctr]



hold <- pe.summ[pe.summ$Prey==preychoice&pe.summ$Light==lightchoice&pe.summ$Fed=='N',]


plot(hold$PAR,hold$ETR,bg=bgvec[as.factor(hold$ExptDay)],pch=21,cex=1.5,xlab='',ylab='',las=1,ylim=c(0,y
Iset <- seq(from = 0, to = 200,length.out=1000)
for(i in 1:length(days)){
  Pmax <- mean(dat[dat$Prey==preychoice&dat$Light==lightchoice&dat$Fed=='N'&dat$ExptDay==days[i],]$Pmax]
  alpha <- mean(dat[dat$Prey==preychoice&dat$Light==lightchoice&dat$Fed=='N'&dat$ExptDay==days[i],]$a)
  # Curves were fit with the Jassby & Platt hyperbolic tangent function:
  # ETR  =  P * tanh(a * PAR / P)

  ETRset <- Pmax*tanh(alpha*Iset/Pmax)
  lines(Iset,ETRset,col=bgvec[i],lwd=3)
}
if(lightctr==3){mtext('PAR (umol quanta m-2 s-1)',side=1,line=2.5,cex=0.8)}
if(preyctr==1){mtext('ETR (e- s-1 chl-a-1)',side=2,line=3,cex=0.8)}
if(lightctr==1){
  if(preyctr==1){mtext(substitute(paste(italic('C. mesostigmatica'))),side=3,line=-1.75,cex=.8)}
  if(preyctr==2){mtext(substitute(paste(italic('H. pacifica'))),side=3,line=-1.75,cex=.8)}
  if(preyctr==3){mtext(substitute(paste(italic('R. salina'))),side=3,line=-1.5,cex=.8)}
  if(preyctr==4){mtext(substitute(paste(italic('S. major'))),side=3,line=-1.75,cex=.8)}

}
  }}
```
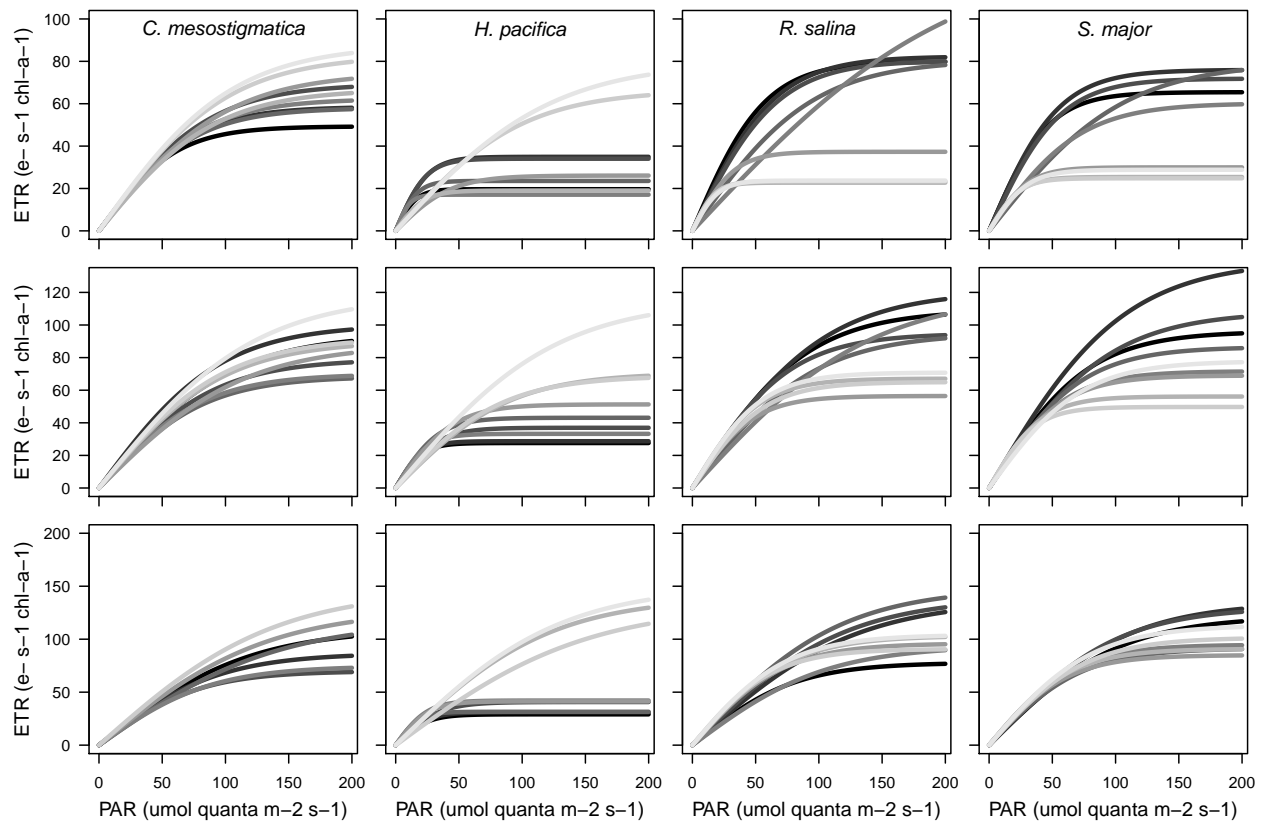
Supplementary Figure: PE curves over time, by prey and light level, measured in carbon fixation per cell

```
dat$Treat.Rep.Day <- paste(dat$Treat.Rep,dat$ExptDay,sep='.')
pe$Treat.Rep.Day <- paste(pe$MCstrain,pe$Prey,pe$Light,pe$Fed,pe$Rep,pe$ExptDay,sep='.')
pe$chl <- dat$corr_chl_p_cell[match(pe$Treat.Rep.Day,dat$Treat.Rep.Day)]
pe$ETR.cell <- pe$ETR.C*as.numeric(as.character(pe$chl))
```

```
## Warning: NAs introduced by coercion
```

```
pe.summ <- summarySE(data=pe,'ETR.cell',groupvars=c('Prey','Light','Fed','ExptDay','PAR'),na.rm=TRUE)
```

```
preychoice_set <- c('CM','HP','RS','SM')
lightchoice_set <- c(10,50,100)
ymax_set <- c(160,160,160)

days <- unique(pe.summ$ExptDay)
bgvec <- rev(c('gray90','gray80','gray70','gray60','gray50','gray40','gray30','gray20','black'))

par(mar=c(1,1,0.5,0.5))
layout(matrix(c(rep(c(13,1,1,1,2,2,2,3,3,3,4,4,4),3),rep(c(13,5,5,5,6,6,6,7,7,7,8,8,8),3),rep(c(13,9,9,9,
```

```
## Warning in matrix(c(rep(c(13, 1, 1, 1, 2, 2, 2, 3, 3, 3, 4, 4, 4), 3),
## rep(c(13, : data length [133] is not a sub-multiple or multiple of the
## number of rows [10]
```

```
for(lightctr in 1:length(lightchoice_set)){
    lightchoice <- lightchoice_set[lightctr]
    ymaxchoice <- ymax_set[lightctr]

for(preyctr in 1:length(preychoice_set)){
  preychoice = preychoice_set[preyctr]



hold <- pe.summ[pe.summ$Prey==preychoice&pe.summ$Light==lightchoice&pe.summ$Fed=='N',]



plot(hold$PAR,hold$ETR.cell,bg=bgvec[as.factor(hold$ExptDay)],pch=21,cex=1.5,xlab='',ylab='',las=1,ylim=
Iset <- seq(from = 0, to = 200,length.out=1000)
for(i in 1:length(days)){
  Pmax <- mean(dat[dat$Prey==preychoice&dat$Light==lightchoice&dat$Fed=='N'&dat$ExptDay==days[i],]$Pmax
  alpha <- mean(dat[dat$Prey==preychoice&dat$Light==lightchoice&dat$Fed=='N'&dat$ExptDay==days[i],]$a)*(
  # Curves were fit with the Jassby & Platt hyperbolic tangent function:
  # ETR  =  P * tanh(a * PAR / P)

  ETRset <- Pmax*tanh(alpha*Iset/Pmax)
  lines(Iset,ETRset,col=bgvec[i],lwd=3)
}
if(lightctr==3){mtext('PAR (umol quanta m-2 s-1)',side=1,line=2.5,cex=0.8)}
if(preyctr==1){mtext('C fix (pg C cell-1 hr-1)',side=2,line=3,cex=0.8)}
if(lightctr==1){
  if(preyctr==1){mtext(substitute(paste(italic('C. mesostigmatica'))),side=3,line=-1.75,cex=.8)}
  if(preyctr==2){mtext(substitute(paste(italic('H. pacifica'))),side=3,line=-1.75,cex=.8)}
  if(preyctr==3){mtext(substitute(paste(italic('R. salina'))),side=3,line=-1.75,cex=.8)}
  if(preyctr==4){mtext(substitute(paste(italic('S. major'))),side=3,line=-1.75,cex=.8)}

}
  }}
```
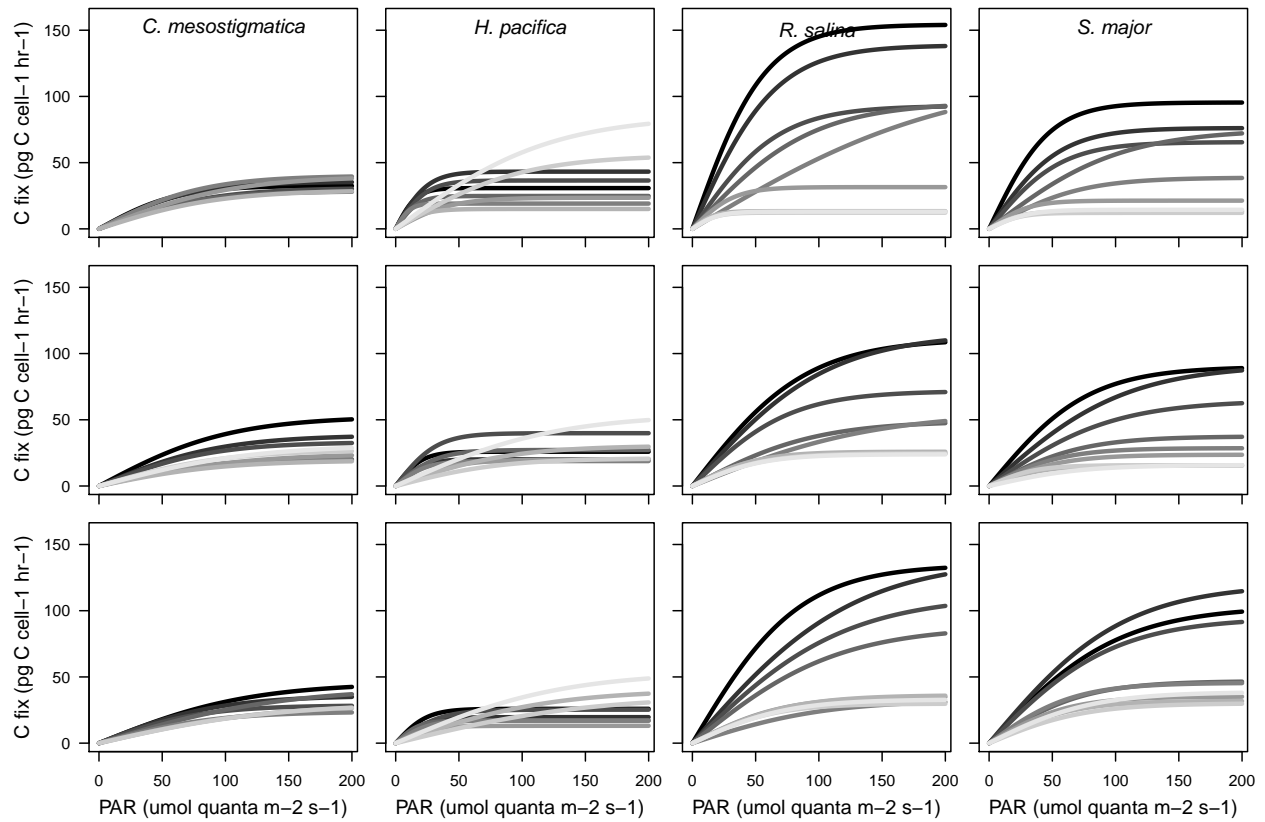
```
## Warning in mean(as.numeric(as.character(dat[dat$Prey == preychoice & dat
## $Light == : NAs introduced by coercion

## Warning in mean(as.numeric(as.character(dat[dat$Prey == preychoice & dat
## $Light == : NAs introduced by coercion
```

Supplementary Figure, Revision: PE curves over time, by prey and light level, measured in carbon fixation per C

```r
dat$Treat.Rep.Day <- paste(dat$Treat.Rep,dat$ExptDay,sep='.')
pe$Treat.Rep.Day <- paste(pe$MCstrain,pe$Prey,pe$Light,pe$Fed,pe$Rep,pe$ExptDay,sep='.')
pe$chl <- dat$corr_chl_p_cell[match(pe$Treat.Rep.Day,dat$Treat.Rep.Day)]
pe$ETR.cell <- pe$ETR.C*as.numeric(as.character(pe$chl))
```

```
## Warning: NAs introduced by coercion
```

```r
pe.summ <- summarySE(data=pe,'ETR.cell',groupvars=c('Prey','Light','Fed','ExptDay','PAR'),na.rm=TRUE)
```

```r
preychoice_set <- c('CM','HP','RS','SM')
lightchoice_set <- c(10,50,100)
ymax_set <- c(250,250,250)

days <- unique(pe.summ$ExptDay)
bgvec <- rev(c('gray90','gray80','gray70','gray60','gray50','gray40','gray30','gray20','black'))

par(mar=c(1,1,0.5,0.5))
layout(matrix(c(rep(c(13,1,1,1,2,2,2,3,3,3,4,4,4),3),rep(c(13,5,5,5,6,6,6,7,7,7,8,8,8),3),rep(c(13,9,9,9
```

```
## Warning in matrix(c(rep(c(13, 1, 1, 1, 2, 2, 2, 3, 3, 3, 4, 4, 4), 3),
## rep(c(13, : data length [133] is not a sub-multiple or multiple of the
## number of rows [10]
```

```r
for(lightctr in 1:length(lightchoice_set)){
    lightchoice <- lightchoice_set[lightctr]
    ymaxchoice <- ymax_set[lightctr]

for(preyctr in 1:length(preychoice_set)){
  preychoice = preychoice_set[preyctr]
  preyC <- mean(carbon[carbon$Prey==preychoice_set[preyctr],]$ngC_cell)




hold <- pe.summ[pe.summ$Prey==preychoice&pe.summ$Light==lightchoice&pe.summ$Fed=='N',]



plot(hold$PAR,hold$ETR.cell/preyC,bg=bgvec[as.factor(hold$ExptDay)],pch=21,cex=1.5,xlab='',ylab='',las=
if(lightctr==3){axis(side=1,labels=T)}else{axis(side=1,labels=F)}; if(preyctr==1){axis(side=2,labels=T,
Iset <- seq(from = 0, to = 200,length.out=1000)
for(i in 1:length(days)){
  Pmax <- mean(dat[dat$Prey==preychoice&dat$Light==lightchoice&dat$Fed=='N'&dat$ExptDay==days[i],]$Pmax
  alpha <- mean(dat[dat$Prey==preychoice&dat$Light==lightchoice&dat$Fed=='N'&dat$ExptDay==days[i],]$a)*
  # Curves were fit with the Jassby & Platt hyperbolic tangent function:
  # ETR  =  P * tanh(a * PAR / P)

  ETRset <- Pmax*tanh(alpha*Iset/Pmax)
  lines(Iset,ETRset,col=bgvec[i],lwd=3)
}
if(lightctr==3){mtext('PAR (umol quanta m-2 s-1)',side=1,line=2.5,cex=0.8)}
if(preyctr==1){mtext('C fix (pg C cell-1 hr-1)',side=2,line=3,cex=0.8)}
if(lightctr==1){
  if(preyctr==1){mtext(substitute(paste(italic('C. mesostigmatica'))),side=3,line=-1.75,cex=.8)}
  if(preyctr==2){mtext(substitute(paste(italic('H. pacifica'))),side=3,line=-1.75,cex=.8)}
  if(preyctr==3){mtext(substitute(paste(italic('R. salina'))),side=3,line=-1.5,cex=.8)}
  if(preyctr==4){mtext(substitute(paste(italic('S. major'))),side=3,line=-1.75,cex=.8)}

}
  }}
```

```
## Warning in mean(as.numeric(as.character(dat[dat$Prey == preychoice & dat
## $Light == : NAs introduced by coercion

## Warning in mean(as.numeric(as.character(dat[dat$Prey == preychoice & dat
## $Light == : NAs introduced by coercion
```
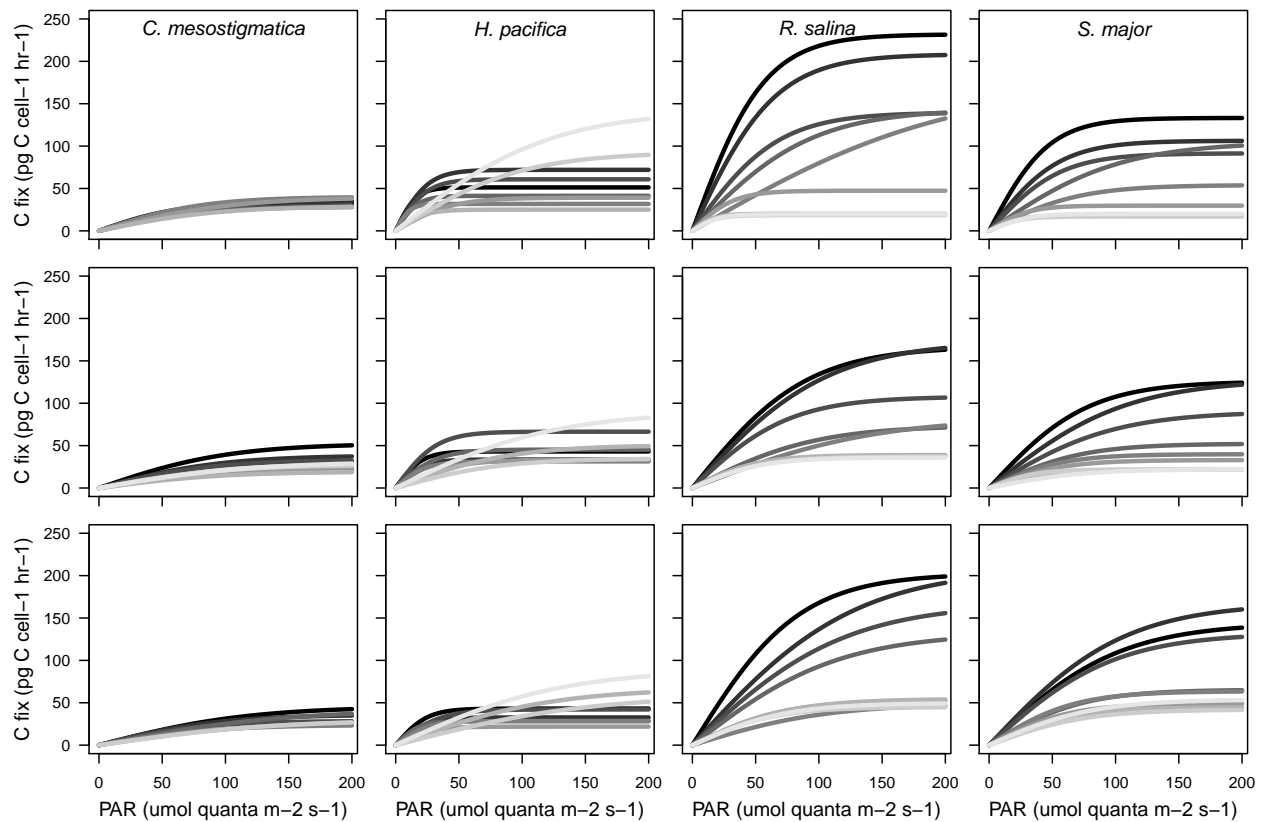
Figure 2: Maximum photosynthetic performance

```
#quartz(height=6.65,width=4)
xcoords <- c(1,2,3,4.5,5.5,6.5,8,9,10,11.5,12.5,13.5)
layout(matrix(c(1,1,2,2,3,3,4,4,5)))
par(mar=c(.5,4,0.5,2))

# Panel A: Fv/Fm
bargraph.CI(Prey,FvFm,group=as.factor(Light),data=MC.max[MC.max$Fed=='Y',],ylim=c(0.35,0.6),las=1,space=

#TukeyHSD(aov(FvFm~as.factor(Light)*Prey,data=MC.max[MC.max$Fed=='Y',]))

# Panel B: P_max per chl
bargraph.CI(Prey,Pmax_chl,group=as.factor(Light),data=MC.max[MC.max$Fed=='Y',],ylim=c(0,15),las=1,space=

#TukeyHSD(aov(Pmax_chl~Prey*as.factor(Light),data=MC.max[MC.max$Fed=='Y',]))

# Panel C: alpha
bargraph.CI(Prey,a,group=as.factor(Light),data=MC.max[MC.max$Fed=='Y',],ylim=c(0,2.5),las=1,space=c(0,0

#TukeyHSD(aov(a~Prey*as.factor(Light),data=MC.max[MC.max$Fed=='Y',]))

# Panel D: P(I) per chl
bargraph.CI(Prey,PI_chl,group=as.factor(Light),data=MC.max[MC.max$Fed=='Y',],las=1,ylim=c(0,9),space=c(

#TukeyHSD(aov(PI_chl~Prey*as.factor(Light),data=MC.max[MC.max$Fed=='Y',]))
```
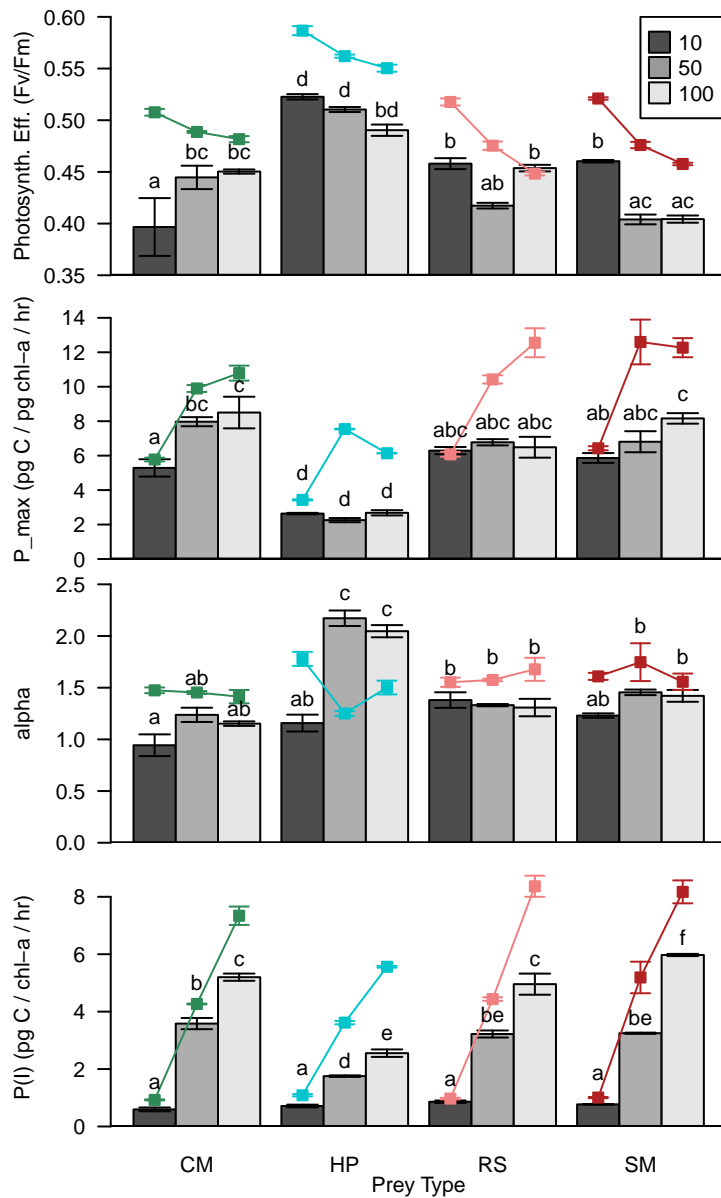
Supplementary Figure: Relative photosynthetic capacity (compared to prey)

```
preytypes <- c('CM','HP','RS','SM'); ptcex <- 1.5
#quartz(width=6.28,height=5.44)
par(mar=c(4,4,0.2,1),mfrow=c(2,2))

plot(MC.max[MC.max$Fed=='Y',]$Light,MC.max[MC.max$Fed=='Y',]$relFvFm,pch=21,bg= preycolvec[MC.max[MC.ma

plot(MC.max[MC.max$Fed=='Y',]$Light,MC.max[MC.max$Fed=='Y',]$rela,pch=21,bg= preycolvec[MC.max[MC.max$Fe

plot(MC.max[MC.max$Fed=='Y',]$Light,MC.max[MC.max$Fed=='Y',]$relPmax_chl,pch=21,bg= preycolvec[MC.max[MC

plot(MC.max[MC.max$Fed=='Y',]$Light,MC.max[MC.max$Fed=='Y',]$relPI_chl,pch=21,bg= preycolvec[MC.max[MC.n
```
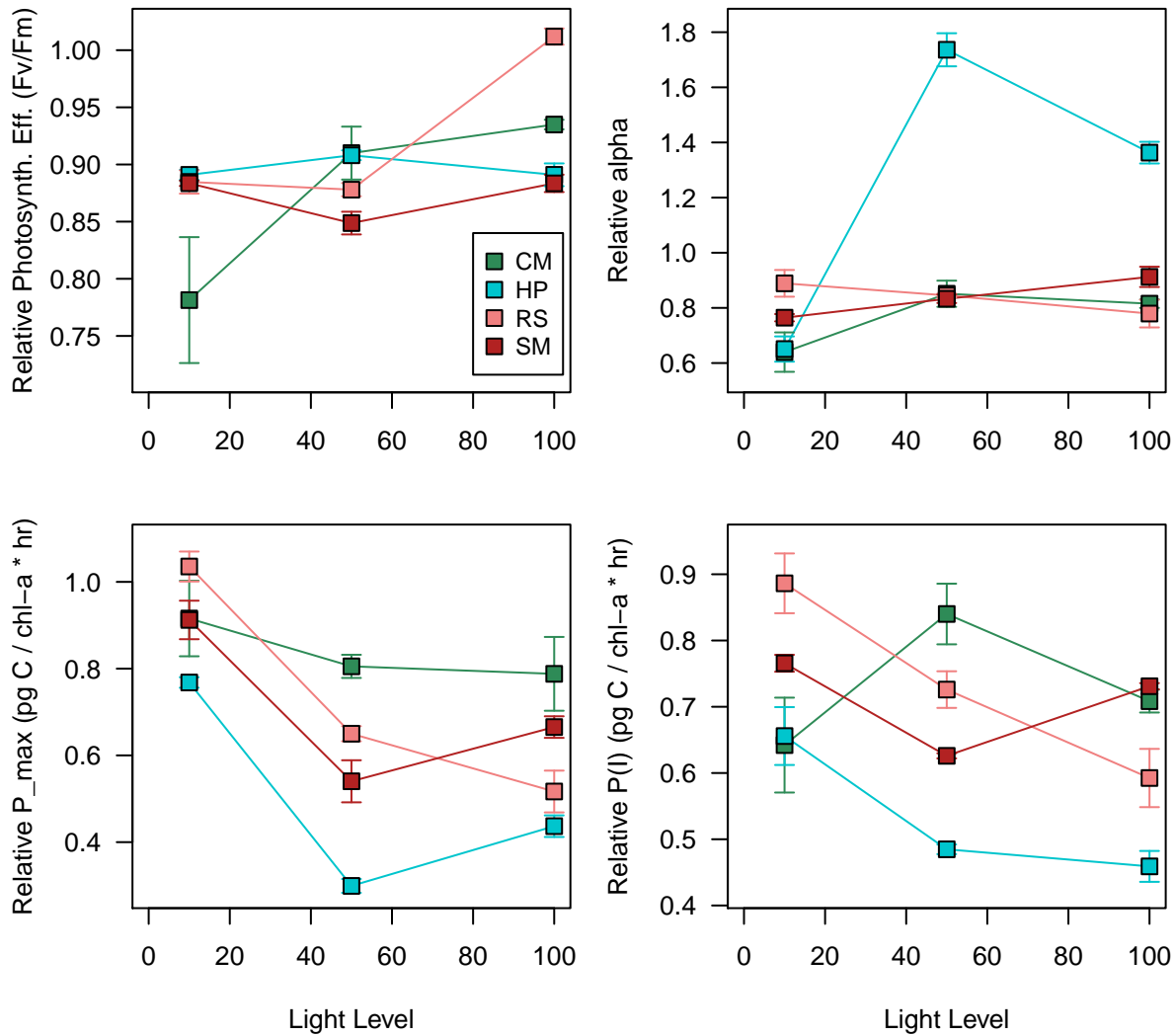
Figure 3: Per-cell plastids, pigment, and C fixation

```
#quartz(height=4.6,width=4.65)
xcoords <- c(1,2,3,4.5,5.5,6.5,8,9,10,11.5,12.5,13.5)
par(mar=c(0.5,4,0.5,4))
layout(matrix(c(1,1,1,2,2,2,3,3,3,4)))

bargraph.CI(Prey,plastids,group=Light,data=MC.max[MC.max$Fed=='Y',],legend=FALSE,x.leg=1,y.leg=15,ylim=c
#TukeyHSD(aov(plastids~as.factor(Light)*Prey,data=MC.max[MC.max$Fed=='Y',]))




# chl-a per cell
bargraph.CI(Prey,chl,group=as.factor(Light),data=MC.max[MC.max$Fed=='Y',],las=1,ylim=c(0,60),space=c(0,0
legend(x = 0.25, y = 55, legend=c('10','50','100'), pch=22,pt.cex=2.5,pt.bg=c('gray30','gray60','gray90
#TukeyHSD(aov(chl~Prey*as.factor(Light),data=MC.max[MC.max$Fed=='Y',]))

# P(I) per cell
```

```
bargraph.CI(Prey,PI_cell,group=as.factor(Light),data=MC.max[MC.max$Fed=='Y',],las=1,ylim=c(0,170),space=
mtext('Prey P(I) (pg C / crypto / hr) ',side=4,line=2,cex=0.7); text(xcoords,c(18,108,118,24,43,43,45,95

#TukeyHSD(aov(PI_cell~Prey*as.factor(Light),data=MC.max[MC.max$Fed=='Y',]))
```
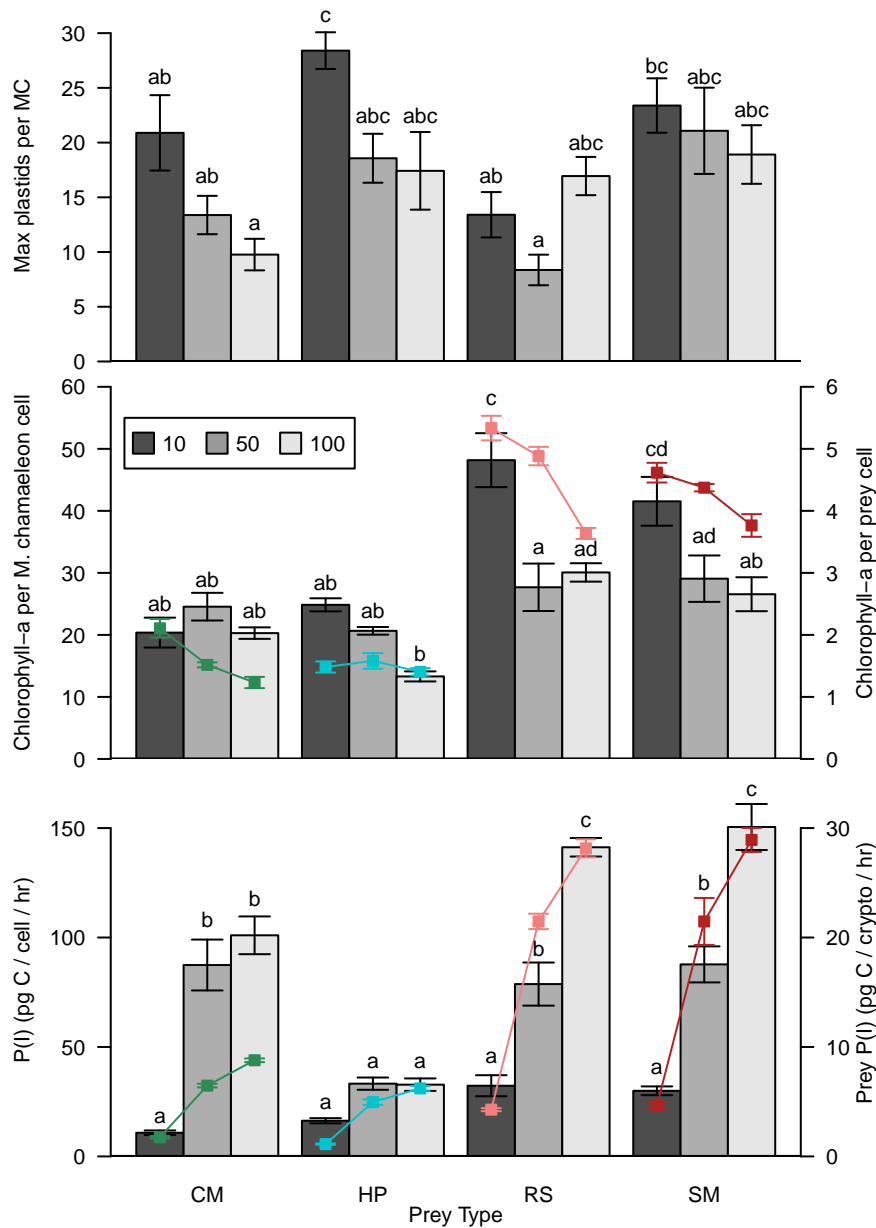

Figure 3, Revised: Per-cell plastids, pigment, and C fixation

```
#quartz(height=4.6,width=4.65)
xcoords <- c(1,2,3,4.5,5.5,6.5,8,9,10,11.5,12.5,13.5)
par(mar=c(0.5,4,0.5,4))
layout(matrix(c(1,1,1,2,2,2,3,3,3,4,4,4,5,5,5,6)))

bargraph.CI(Prey,plastids,group=Light,data=MC.max[MC.max$Fed=='Y',],legend=FALSE,x.leg=1,y.leg=15,ylim=c
```

```r
#TukeyHSD(aov(plastids~as.factor(Light)*Prey,data=MC.max[MC.max$Fed=='Y',]))




# chl-a per cell
bargraph.CI(Prey,chl,group=as.factor(Light),data=MC.max[MC.max$Fed=='Y',],las=1,ylim=c(0,60),space=c(0,
legend(x = 0.25, y = 55, legend=c('10','50','100'), pch=22,pt.cex=2.5,pt.bg=c('gray30','gray60','gray90
#TukeyHSD(aov(chl~Prey*as.factor(Light),data=MC.max[MC.max$Fed=='Y',]))

# P(I) per cell
bargraph.CI(Prey,PI_cell,group=as.factor(Light),data=MC.max[MC.max$Fed=='Y',],las=1,ylim=c(0,170),space=
mtext('Prey P(I) (pg C / crypto / hr) ',side=4,line=2.2,cex=0.7); text(xcoords,c(18,108,118,24,43,43,45

#TukeyHSD(aov(PI_cell~Prey*as.factor(Light),data=MC.max[MC.max$Fed=='Y',]))

# chl per C
bargraph.CI(Prey,ChlperC,group=as.factor(Light),data=MC.max[MC.max$Fed=='Y',],las=1,ylim=c(0,90),space=
text(xcoords,c(26,31,24,48,39,28,85,52,52,68,50,55),c('a','ab','a',    'bc','ab','a',    'd','bc','c',
#TukeyHSD(aov(ChlperC~as.factor(Light)*Prey,data=MC.max[MC.max$Fed=='Y',]))

# P(I) per C
bargraph.CI(Prey,PI_C,group=as.factor(Light),data=MC.max[MC.max$Fed=='Y',],las=1,ylim=c(0,250),space=c(
mtext('Prey P(I) (pg C / crypto / hr) ',side=4,line=2.5,cex=0.7); text(xcoords,c(38,115,128,40,83,73,70

#TukeyHSD(aov(PI_cell~Prey*as.factor(Light),data=MC.max[MC.max$Fed=='Y',]))
```
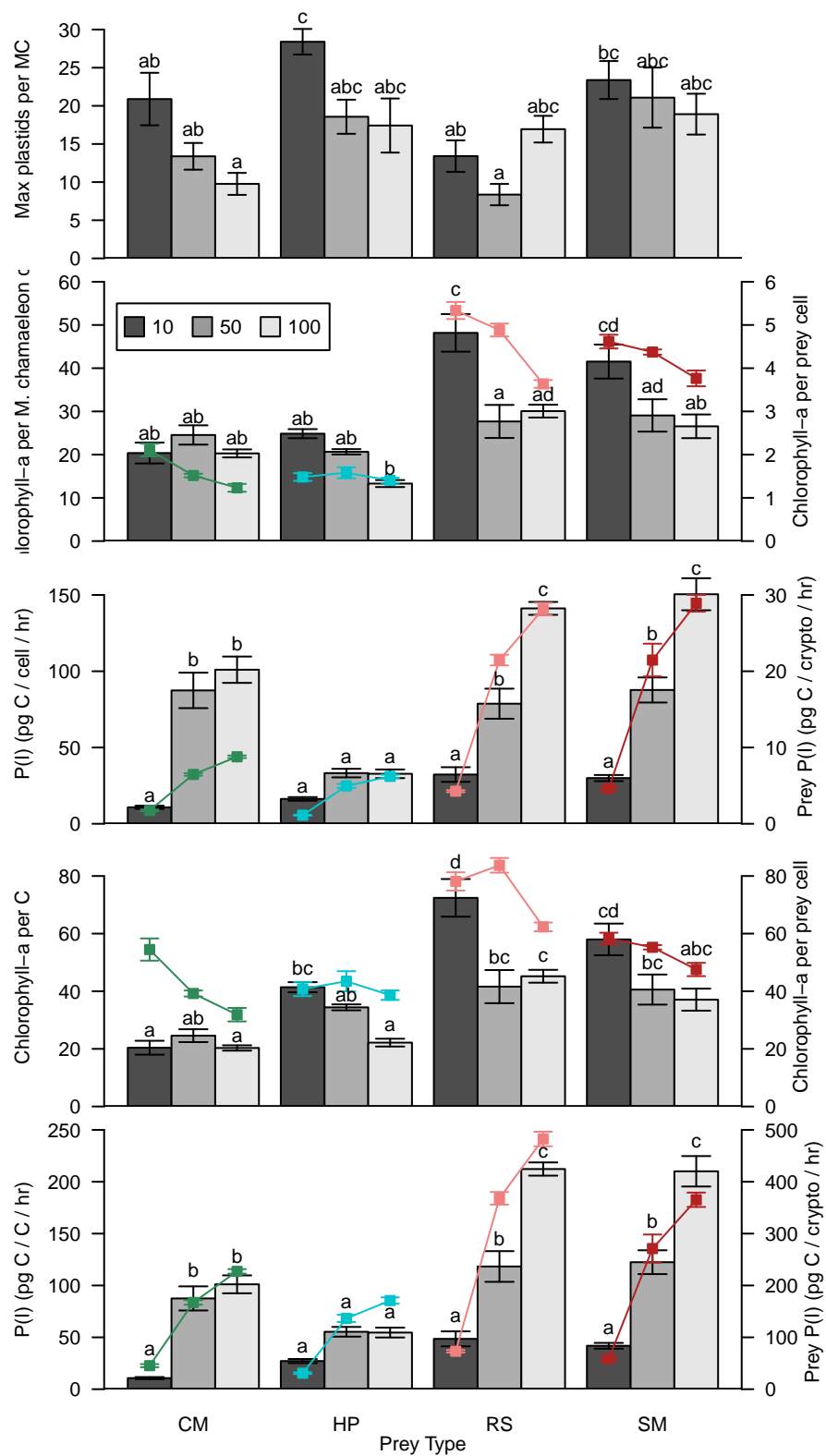
Figure 4: Growth rate and extent

```r
growth.summ<-summarySE(data=growth,measurevar='muMC',groupvars=c('Prey','Light','Fed'))
growth$Prey.Light <- paste(growth$Prey,growth$Light,sep='.')
prey.growth.summ <- summarySE(data=growth[growth$Fed=='Y',],measurevar='muPreyCtrl',groupvars=c('Prey',

xcoords <- c(1.2,3.4,5.6)
xcoords2 <- c(.7,1.7,2.9,3.9,5.1,6.1)
#quartz(height=3.5,width=7.5)
par(mar=c(1,1,0.5,0.5))
layout(matrix(c(11,1,1,1,2,2,2,3,3,3,4,4,4,9,9,9,9,9,9,10,5,5,5,6,6,6,7,7,7,8,8,8,9,9,9,9,9,9),nrow=2,n

# Column 1: Growth Rate
ymax <- 1.2; ymin <- -0.1; bargraph.CI(Light,muMC,group=Fed,data=growth[growth$Prey=='CM',],las=1,legend

bargraph.CI(Light,muMC,group=Fed,data=growth[growth$Prey=='HP',],las=1,legend=FALSE,leg.lab=c('Starved'

bargraph.CI(Light,muMC,group=Fed,data=growth[growth$Prey=='RS',],las=1,legend=FALSE,leg.lab=c('Starved'

bargraph.CI(Light,muMC,group=Fed,data=growth[growth$Prey=='SM',],las=1,legend=FALSE,leg.lab=c('Starved'

# Row 2: growth extent
xlabelstr <- '10uE          50uE          100uE'
ymax <- 12.4; ymin <- 0; bargraph.CI(Light,relincrease,group=Fed,data=growth[growth$Prey=='CM',],las=1,

## Warning in arrows(xvals[, i], if (lc) CI.L[, i] else mn.data[, i],
## xvals[, : zero-length arrow is of indeterminate angle and so skipped

bargraph.CI(Light,relincrease,group=Fed,data=growth[growth$Prey=='HP',],las=1,legend=FALSE,leg.lab=c('S

bargraph.CI(Light, relincrease,group=Fed,data=growth[growth$Prey=='RS',],las=1,legend=FALSE,leg.lab=c('S

bargraph.CI(Light, relincrease,group=Fed,data=growth[growth$Prey=='SM',],las=1,legend=FALSE,leg.lab=c('S


par(mar=c(4,5,0.1,0.1))
ptcex <- 2

# First panel: growth rate vs. growth extent

lm.all <- lm(growth$relincrease~growth$muMC); summary(lm.all) #signif.; F-stat = 86.4, p-val = 7.616e-1

##
## Call:
## lm(formula = growth$relincrease ~ growth$muMC)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -3.8268 -1.0467 -0.4266  1.0790  5.4003
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)   0.1771     0.4529   0.391    0.697
```

```
## growth$muMC  13.0391     1.4028   9.295 7.62e-14 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.892 on 70 degrees of freedom
## Multiple R-squared:  0.5524, Adjusted R-squared:  0.546
## F-statistic:  86.4 on 1 and 70 DF,  p-value: 7.616e-14
```

```r
lm.RS <- lm(relincrease~muMC,data=growth[growth$Prey=='RS',]); summary(lm.RS) #signif.; F-stat = 39.13,
```

```
##
## Call:
## lm(formula = relincrease ~ muMC, data = growth[growth$Prey ==
##     "RS", ])
##
## Residuals:
##     Min     1Q  Median     3Q     Max
## -3.1669 -1.3449  0.3205  1.3619  3.3652
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)   -1.942      1.262  -1.539    0.143
## muMC          21.457      3.430   6.255 1.15e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.951 on 16 degrees of freedom
## Multiple R-squared:  0.7098, Adjusted R-squared:  0.6916
## F-statistic: 39.13 on 1 and 16 DF,  p-value: 1.148e-05
```

```r
lm.SM <- lm(relincrease~muMC,data=growth[growth$Prey=='SM',]); summary(lm.SM) #signif.; F-stat = 36.33,
```

```
##
## Call:
## lm(formula = relincrease ~ muMC, data = growth[growth$Prey ==
##     "SM", ])
##
## Residuals:
##     Min     1Q  Median     3Q     Max
## -2.3789 -0.6495 -0.1635  0.4765  2.4325
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  -0.1947     0.7310  -0.266    0.793
## muMC         13.2977     2.2061   6.028 1.76e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.194 on 16 degrees of freedom
## Multiple R-squared:  0.6943, Adjusted R-squared:  0.6752
## F-statistic: 36.33 on 1 and 16 DF,  p-value: 1.758e-05
```

```r
lm.CM <- lm(relincrease~muMC,data=growth[growth$Prey=='CM',]); summary(lm.CM) #signif.; F-stat = 138.7,
```

```
##
## Call:
```

```
## lm(formula = relincrease ~ muMC, data = growth[growth$Prey ==
##      "CM", ])
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -1.7871 -0.4654 -0.2081  0.5969  2.0592
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)   0.9255     0.3480   2.659   0.0171 *
## muMC         16.1727     1.3733  11.777  2.7e-09 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.054 on 16 degrees of freedom
## Multiple R-squared:  0.8966, Adjusted R-squared:  0.8901
## F-statistic: 138.7 on 1 and 16 DF,  p-value: 2.7e-09
```

```r
lm.HP <- lm(relincrease~muMC,data=growth[growth$Prey=='HP',]); summary(lm.HP) #signif.; F-stat = 45.33,
```

```
##
## Call:
## lm(formula = relincrease ~ muMC, data = growth[growth$Prey ==
##      "HP", ])
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.82467 -0.28724  0.00287  0.15622  1.06984
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)   0.5010     0.2923   1.714    0.106
## muMC          5.9977     0.8908   6.733 4.81e-06 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.5175 on 16 degrees of freedom
## Multiple R-squared:  0.7391, Adjusted R-squared:  0.7228
## F-statistic: 45.33 on 1 and 16 DF,  p-value: 4.81e-06
```

```r
plot(growth$muMC,growth$relincrease,pch=c(21,22,24)[as.factor(growth$Light)],bg=c(CMcol,HPcol,RScol,SMco
```

```
## Warning in arrows(C.summ[, 5], I.summ[, 5] + I.summ$se, C.summ[, 5],
## I.summ[, : zero-length arrow is of indeterminate angle and so skipped
```

```r
#legend(x = -0.15, y = 12, legend = c('0 uE','50 uE','100 uE','CM','HP',"RS","SM"),cex=ptcex,pt.cex=1.5
```
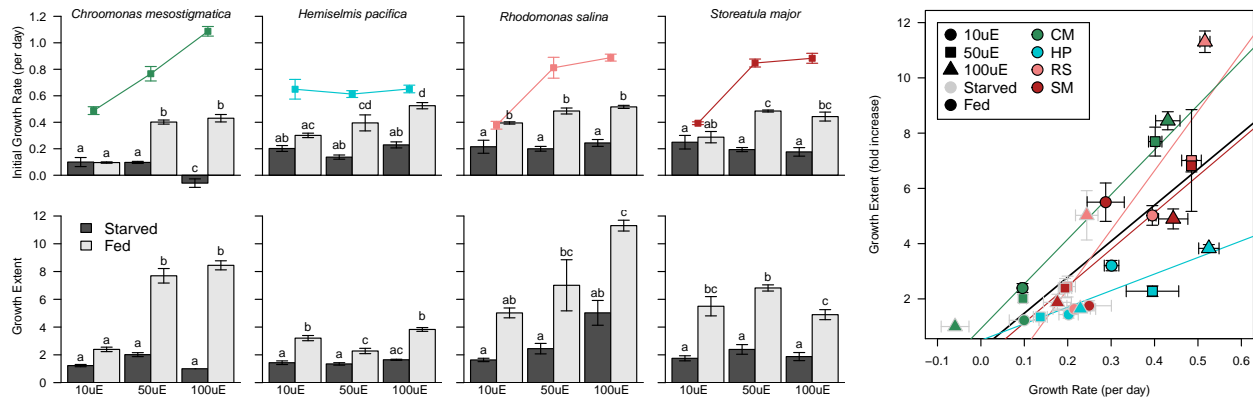
Figure 5: Heterotrophic contributions to growth

```r
#layout(matrix(c(1,1,1,2,2,2,8,3,3,3,4,4,4,7,5,5,5,6,6,6,9),nrow=(6*3+3),ncol=1))
layout(matrix(c(1,1,1,2,2,3,3,3,4,4),nrow=2,ncol=5,byrow=TRUE))
xcoords <- c(1,2,3,4.5,5.5,6.5,8,9,10,11.5,12.5,13.5)




# ingestion rate
par(mar=c(2,4,0.5,0.5))
bargraph.CI(Prey,ingest_2,group=Light,data=growth[growth$Fed=='Y',],legend=FALSE,x.leg=1,y.leg=15,ylim=

par(mar=c(4,4,1,0.5))

# SECOND PLOT: ingestion rate vs growth rate
lm.all <- lm(growth[growth$Fed=='Y',]$muMC~growth[growth$Fed=='Y',]$ingest_2); summary(lm.all) #signif.
```

```
##
## Call:
## lm(formula = growth[growth$Fed == "Y", ]$muMC ~ growth[growth$Fed ==
##     "Y", ]$ingest_2)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.27035 -0.04367  0.01011  0.07994  0.16933
##
## Coefficients:
##                                 Estimate Std. Error t value Pr(>|t|)
## (Intercept)                     0.266463   0.042546   6.263 3.93e-07
## growth[growth$Fed == "Y", ]$ingest_2 0.017805   0.005259   3.386   0.0018
##
## (Intercept)                              ***
## growth[growth$Fed == "Y", ]$ingest_2 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.1089 on 34 degrees of freedom
## Multiple R-squared:  0.2522, Adjusted R-squared:  0.2302
## F-statistic: 11.46 on 1 and 34 DF,  p-value: 0.001805
```

```
lm.RS <- lm(muMC~ingest_2,data=growth[growth$Prey=='RS'&growth$Fed=='Y',]); summary(lm.RS) #signif.; F-

##
## Call:
## lm(formula = muMC ~ ingest_2, data = growth[growth$Prey == "RS" &
##     growth$Fed == "Y", ])
##
## Residuals:
##       Min        1Q    Median        3Q       Max
## -0.085170 -0.056651  0.008239  0.059667  0.068218
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) 0.459887   0.081843   5.619   0.0008 ***
## ingest_2    0.000672   0.009708   0.069   0.9468
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.06338 on 7 degrees of freedom
## Multiple R-squared:  0.000684,   Adjusted R-squared:  -0.1421
## F-statistic: 0.004791 on 1 and 7 DF,  p-value: 0.9468

lm.SM <- lm(muMC~ingest_2,data=growth[growth$Prey=='SM'&growth$Fed=='Y',]); summary(lm.SM) #signif.; F-

##
## Call:
## lm(formula = muMC ~ ingest_2, data = growth[growth$Prey == "SM" &
##     growth$Fed == "Y", ])
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.07256 -0.05838  0.00850  0.05436  0.08521
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) 0.189548   0.067162   2.822   0.0257 *
## ingest_2    0.020717   0.006088   3.403   0.0114 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.06686 on 7 degrees of freedom
## Multiple R-squared:  0.6233, Adjusted R-squared:  0.5694
## F-statistic: 11.58 on 1 and 7 DF,  p-value: 0.0114

lm.CM <- lm(muMC~ingest_2,data=growth[growth$Prey=='CM'&growth$Fed=='Y',]); summary(lm.CM) #signif.; F-

##
## Call:
## lm(formula = muMC ~ ingest_2, data = growth[growth$Prey == "CM" &
##     growth$Fed == "Y", ])
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.21576 -0.15231  0.01321  0.11083  0.16924
##
```

```
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  0.18688    0.11165   1.674    0.138
## ingest_2     0.02215    0.01782   1.243    0.254
##
## Residual standard error: 0.1578 on 7 degrees of freedom
## Multiple R-squared:  0.1808, Adjusted R-squared:  0.06382
## F-statistic: 1.545 on 1 and 7 DF,  p-value: 0.2538
```

```r
lm.HP <- lm(muMC~ingest_2,data=growth[growth$Prey=='HP'&growth$Fed=='Y',]); summary(lm.HP) #signif.; F-
```

```
##
## Call:
## lm(formula = muMC ~ ingest_2, data = growth[growth$Prey == "HP" &
##     growth$Fed == "Y", ])
##
## Residuals:
##       Min        1Q    Median        3Q       Max
## -0.094714 -0.028945  0.006322  0.040034  0.071321
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  0.12162    0.06364   1.911  0.09763 .
## ingest_2     0.05503    0.01166   4.720  0.00216 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.0593 on 7 degrees of freedom
## Multiple R-squared:  0.7609, Adjusted R-squared:  0.7267
## F-statistic: 22.27 on 1 and 7 DF,  p-value: 0.002159
```

```r
plot(growth[growth$Fed=='Y',]$ingest_2,growth[growth$Fed=='Y',]$muMC,las=1,pch=c(21,22,24)[as.factor(gr
C.summ <- summarySE(data=growth[growth$Fed=='Y',],measurevar='muMC',groupvars=c('Light','Prey')); I.summ

legend(13.1,0.29,legend=c('10uE','50uE','100uE'),pch=c(21,22,24),pt.cex=ptcex,pt.bg='black',col='black'



# linear scale: prey per initial MC
par(mar=c(2,4,0.5,0.5))
bargraph.CI(Prey,(PreyperMC),group=Light,data=growth[growth$Fed=='Y',],legend=FALSE,err.width=0.05,names


# FOURTH PLOT: total ingestion vs growth extent

par(mar=c(4,4,1,0.5))
growth.y <- growth[growth$Fed=='Y',]
lm.all <- lm(growth.y$relincrease~log(growth.y$PreyperMC)); summary(lm.all) #signif.; F-stat = 8.4, p-v
```

```
##
## Call:
## lm(formula = growth.y$relincrease ~ log(growth.y$PreyperMC))
##
## Residuals:
##      Min       1Q   Median       3Q      Max
```

```
## -3.4740 -1.2625 -0.4977  0.6485  6.5826
##
## Coefficients:
##                          Estimate Std. Error t value Pr(>|t|)
## (Intercept)                0.6685     1.7857   0.374  0.71047
## log(growth.y$PreyperMC)    1.4408     0.4971   2.898  0.00652 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2.511 on 34 degrees of freedom
## Multiple R-squared:  0.1981, Adjusted R-squared:  0.1745
## F-statistic:   8.4 on 1 and 34 DF,  p-value: 0.006525
```

```r
lm.RS.f <- lm(relincrease~log(PreyperMC),data=growth.y[growth.y$Prey=='RS'&growth.y$Fed=='Y',]); summary
```

```
##
## Call:
## lm(formula = relincrease ~ log(PreyperMC), data = growth.y[growth.y$Prey ==
##     "RS" & growth.y$Fed == "Y", ])
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -4.0784 -1.4995 -0.8877  2.9664  4.1790
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    -9.476     11.599  -0.817    0.441
## log(PreyperMC)  5.606      3.754   1.493    0.179
##
## Residual standard error: 3.016 on 7 degrees of freedom
## Multiple R-squared:  0.2416, Adjusted R-squared:  0.1333
## F-statistic:  2.23 on 1 and 7 DF,  p-value: 0.179
```

```r
lm.SM.f <- lm(relincrease~log(PreyperMC),data=growth.y[growth.y$Prey=='SM'&growth.y$Fed=='Y',]); summary
```

```
##
## Call:
## lm(formula = relincrease ~ log(PreyperMC), data = growth.y[growth.y$Prey ==
##     "SM" & growth.y$Fed == "Y", ])
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.45464 -0.81082  0.05431  0.65520  1.45024
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)     1.056      4.534   0.233    0.823
## log(PreyperMC)  1.380      1.332   1.036    0.335
##
## Residual standard error: 1.1 on 7 degrees of freedom
## Multiple R-squared:  0.133,  Adjusted R-squared:  0.009104
## F-statistic: 1.073 on 1 and 7 DF,  p-value: 0.3346
```

```r
lm.CM.f <- lm(relincrease~log(PreyperMC),data=growth.y[growth.y$Prey=='CM'&growth.y$Fed=='Y',]); summary
```

```
##
```

```
## Call:
## lm(formula = relincrease ~ log(PreyperMC), data = growth.y[growth.y$Prey ==
##     "CM" & growth.y$Fed == "Y", ])
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.96250 -0.71021 -0.18499 -0.08223  1.92060
##
## Coefficients:
##                Estimate Std. Error t value Pr(>|t|)
## (Intercept)     -4.5418     1.6693  -2.721 0.029730 *
## log(PreyperMC)   2.3742     0.3597   6.601 0.000304 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.158 on 7 degrees of freedom
## Multiple R-squared:  0.8616, Adjusted R-squared:  0.8418
## F-statistic: 43.57 on 1 and 7 DF,  p-value: 0.0003041
```

```r
lm.HP.f <- lm(relincrease~log(PreyperMC),data=growth.y[growth.y$Prey=='HP'&growth.y$Fed=='Y',]); summary
```

```
##
## Call:
## lm(formula = relincrease ~ log(PreyperMC), data = growth.y[growth.y$Prey ==
##     "HP" & growth.y$Fed == "Y", ])
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -0.8070 -0.2609 -0.0068  0.2690  0.7411
##
## Coefficients:
##                Estimate Std. Error t value Pr(>|t|)
## (Intercept)      9.4956     2.5353   3.745  0.00721 **
## log(PreyperMC)  -2.1434     0.8479  -2.528  0.03936 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.5596 on 7 degrees of freedom
## Multiple R-squared:  0.4772, Adjusted R-squared:  0.4025
## F-statistic:  6.39 on 1 and 7 DF,  p-value: 0.03936
```

```r
plot(log(as.numeric(as.character(growth.y$PreyperMC))),growth.y$relincrease,pch=c(21,22,24)[as.factor(g
```
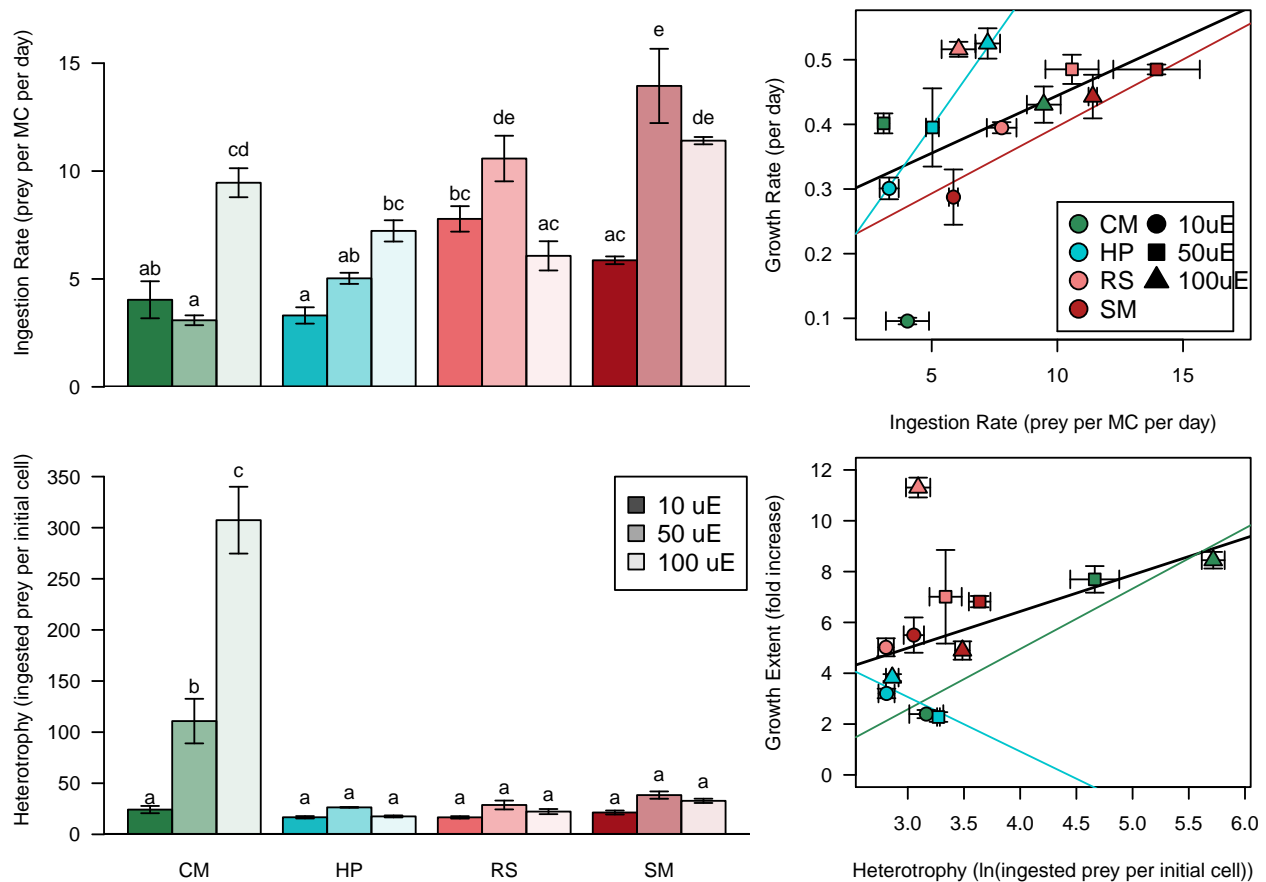
```
#legend(1050,12.2,legend=c('CM','HP','RS','SM'),pch=21,pt.cex=ptcex,pt.bg=preycolvec,bty='n'); arrows(c
```

Figure 5, revision: Heterotrophic contributions to growth

```
#layout(matrix(c(1,1,1,2,2,2,8,3,3,3,4,4,4,7,5,5,5,6,6,6,9),nrow=(6*3+3),ncol=1))
layout(matrix(c(1,1,1,2,2,3,3,3,4,4),nrow=2,ncol=5,byrow=TRUE))
xcoords <- c(1,2,3,4.5,5.5,6.5,8,9,10,11.5,12.5,13.5)



# ingestion rate
par(mar=c(2,4,0.5,0.5))
bargraph.CI(Prey,ingest_2,group=Light,data=growth[growth$Fed=='Y',],legend=FALSE,x.leg=1,y.leg=15,ylim=c

par(mar=c(4,4,1,0.5))

# SECOND PLOT: ingestion rate vs growth rate
# Revision: convert to per carbon
carbon$Prey.Rep <- paste(carbon$Prey,carbon$Rep,sep='.')
carbon$Sp.Rep <- paste(carbon$Species,carbon$Rep,sep='.')
growth$Prey.Rep <- paste(growth$Prey,growth$Rep,sep='.')
growth$MC.C <- carbon[carbon$Species=='MC',]$ngC_cell[match(growth$Prey.Rep,carbon[carbon$Species=='MC'
growth$prey.C <- carbon[carbon$Species!='MC',]$ngC_cell[match(growth$Prey.Rep,carbon[carbon$Species!='MC
```

```
growth$preyCperMCperday <- growth$ingest_2*growth$prey.C/growth$MC.C
growth$heterotrophy.C <- growth$PreyperMC*growth$prey.C/growth$MC.C

lm.all <- lm(growth[growth$Fed=='Y',]$muMC~growth[growth$Fed=='Y',]$preyCperMCperday); summary(lm.all)
```

```
##
## Call:
## lm(formula = growth[growth$Fed == "Y", ]$muMC ~ growth[growth$Fed ==
##     "Y", ]$preyCperMCperday)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.25597 -0.06217  0.02526  0.07555  0.17508
##
## Coefficients:
##                                          Estimate Std. Error t value
## (Intercept)                               0.32865    0.03136   10.48
## growth[growth$Fed == "Y", ]$preyCperMCperday  0.11187    0.04098    2.73
##                                          Pr(>|t|)
## (Intercept)                               3.46e-12 ***
## growth[growth$Fed == "Y", ]$preyCperMCperday  0.00996 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.1141 on 34 degrees of freedom
## Multiple R-squared:  0.1798, Adjusted R-squared:  0.1557
## F-statistic: 7.454 on 1 and 34 DF,  p-value: 0.009955
```

```
lm.RS <- lm(muMC~preyCperMCperday,data=growth[growth$Prey=='RS'&growth$Fed=='Y',]); summary(lm.RS) #n.s
```

```
##
## Call:
## lm(formula = muMC ~ preyCperMCperday, data = growth[growth$Prey ==
##     "RS" & growth$Fed == "Y", ])
##
## Residuals:
##       Min        1Q    Median        3Q       Max
## -0.085490 -0.059006  0.004134  0.052806  0.070208
##
## Coefficients:
##                  Estimate Std. Error t value Pr(>|t|)
## (Intercept)       0.45052    0.06457   6.977 0.000216 ***
## preyCperMCperday  0.02013    0.08278   0.243 0.814840
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.06314 on 7 degrees of freedom
## Multiple R-squared:  0.008377,   Adjusted R-squared:  -0.1333
## F-statistic: 0.05914 on 1 and 7 DF,  p-value: 0.8148
```

```
lm.SM <- lm(muMC~preyCperMCperday,data=growth[growth$Prey=='SM'&growth$Fed=='Y',]); summary(lm.SM) #sig
```

```
##
## Call:
## lm(formula = muMC ~ preyCperMCperday, data = growth[growth$Prey ==
```

```
##     "SM" & growth$Fed == "Y", ])
##
## Residuals:
##       Min       1Q    Median        3Q       Max
## -0.089937 -0.058651 -0.009645  0.053621  0.085126
##
## Coefficients:
##                 Estimate Std. Error t value Pr(>|t|)
## (Intercept)      0.21793    0.06763   3.222   0.0146 *
## preyCperMCperday 0.16037    0.05410   2.964   0.0210 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.07253 on 7 degrees of freedom
## Multiple R-squared:  0.5566, Adjusted R-squared:  0.4932
## F-statistic: 8.786 on 1 and 7 DF,  p-value: 0.02098
```

```
lm.CM <- lm(muMC~preyCperMCperday,data=growth[growth$Prey=='CM'&growth$Fed=='Y',]); summary(lm.CM) #n.s
```

```
##
## Call:
## lm(formula = muMC ~ preyCperMCperday, data = growth[growth$Prey ==
##     "CM" & growth$Fed == "Y", ])
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -0.2038 -0.1670  0.0300  0.1156  0.1690
##
## Coefficients:
##                 Estimate Std. Error t value Pr(>|t|)
## (Intercept)       0.1974     0.1066   1.852    0.106
## preyCperMCperday  0.5200     0.4302   1.209    0.266
##
## Residual standard error: 0.1585 on 7 degrees of freedom
## Multiple R-squared:  0.1727, Adjusted R-squared:  0.0545
## F-statistic: 1.461 on 1 and 7 DF,  p-value: 0.266
```

```
lm.HP <- lm(muMC~preyCperMCperday,data=growth[growth$Prey=='HP'&growth$Fed=='Y',]); summary(lm.HP) #sig
```

```
##
## Call:
## lm(formula = muMC ~ preyCperMCperday, data = growth[growth$Prey ==
##     "HP" & growth$Fed == "Y", ])
##
## Residuals:
##       Min       1Q    Median        3Q       Max
## -0.095104 -0.023532  0.002273  0.042511  0.052887
##
## Coefficients:
##                 Estimate Std. Error t value Pr(>|t|)
## (Intercept)      0.12936    0.05598   2.311  0.05412 .
## preyCperMCperday 0.88395    0.16847   5.247  0.00119 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
```

```
## Residual standard error: 0.0546 on 7 degrees of freedom
## Multiple R-squared:  0.7973, Adjusted R-squared:  0.7683
## F-statistic: 27.53 on 1 and 7 DF,  p-value: 0.00119
```

```r
plot(growth[growth$Fed=='Y',]$preyCperMCperday,growth[growth$Fed=='Y',]$muMC,las=1,pch=c(21,22,24)[as.fa
C.summ <- summarySE(data=growth[growth$Fed=='Y',],measurevar='muMC',groupvars=c('Light','Prey')); I.summ

legend(1.5,0.29,legend=c('10uE','50uE','100uE'),pch=c(21,22,24),pt.cex=ptcex,pt.bg='black',col='black',l
```

```r
# linear scale: prey per initial MC
par(mar=c(2,4,0.5,0.5))
bargraph.CI(Prey,(PreyperMC),group=Light,data=growth[growth$Fed=='Y',],legend=FALSE,err.width=0.05,names
```

```r
# FOURTH PLOT: total ingestion vs growth extent

par(mar=c(4,4,1,0.5))
growth.y <- growth[growth$Fed=='Y',]
lm.all <- lm(growth.y$relincrease~log(growth.y$heterotrophy.C)); summary(lm.all) #signif.; F-stat = 8.4
```

```
##
## Call:
## lm(formula = growth.y$relincrease ~ log(growth.y$heterotrophy.C))
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -3.0097 -1.0832 -0.4442  0.0672  6.0001
##
## Coefficients:
##                             Estimate Std. Error t value Pr(>|t|)
## (Intercept)                   3.9082     0.5595   6.986 4.66e-08 ***
## log(growth.y$heterotrophy.C)  2.1809     0.5048   4.320 0.000128 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2.253 on 34 degrees of freedom
## Multiple R-squared:  0.3544, Adjusted R-squared:  0.3354
## F-statistic: 18.66 on 1 and 34 DF,  p-value: 0.0001283
```

```r
lm.RS.f <- lm(relincrease~log(heterotrophy.C),data=growth.y[growth.y$Prey=='RS'&growth.y$Fed=='Y',]); su
```

```
##
## Call:
## lm(formula = relincrease ~ log(heterotrophy.C), data = growth.y[growth.y$Prey ==
##     "RS" & growth.y$Fed == "Y", ])
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -2.9145 -2.3739 -0.1336  2.7505  4.2343
##
## Coefficients:
##                     Estimate Std. Error t value Pr(>|t|)
## (Intercept)            4.890      2.185   2.238   0.0602 .
```

```
## log(heterotrophy.C)     4.434       2.977   1.490    0.1799
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 3.018 on 7 degrees of freedom
## Multiple R-squared:  0.2407, Adjusted R-squared:  0.1322
## F-statistic: 2.219 on 1 and 7 DF,  p-value: 0.1799
```

lm.SM.f <- **lm**(relincrease~**log**(heterotrophy.C),data=growth.y[growth.y$Prey=='SM'&growth.y$Fed=='Y',]); su

```
##
## Call:
## lm(formula = relincrease ~ log(heterotrophy.C), data = growth.y[growth.y$Prey ==
##      "SM" & growth.y$Fed == "Y", ])
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -1.5741 -0.9955  0.1905  0.8409  1.3864
##
## Coefficients:
##                     Estimate Std. Error t value Pr(>|t|)
## (Intercept)            4.217      1.657   2.544   0.0384 *
## log(heterotrophy.C)    1.270      1.348   0.942   0.3777
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.113 on 7 degrees of freedom
## Multiple R-squared:  0.1125, Adjusted R-squared:  -0.01434
## F-statistic: 0.8869 on 1 and 7 DF,  p-value: 0.3777
```

lm.CM.f <- **lm**(relincrease~**log**(heterotrophy.C),data=growth.y[growth.y$Prey=='CM'&growth.y$Fed=='Y',]); su

```
##
## Call:
## lm(formula = relincrease ~ log(heterotrophy.C), data = growth.y[growth.y$Prey ==
##      "CM" & growth.y$Fed == "Y", ])
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.09514 -0.70175 -0.09685  0.09738  1.93986
##
## Coefficients:
##                     Estimate Std. Error t value Pr(>|t|)
## (Intercept)           3.2257     0.5928   5.441 0.000965 ***
## log(heterotrophy.C)   2.3409     0.3560   6.576 0.000311 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.161 on 7 degrees of freedom
## Multiple R-squared:  0.8607, Adjusted R-squared:  0.8408
## F-statistic: 43.25 on 1 and 7 DF,  p-value: 0.0003111
```

lm.HP.f <- **lm**(relincrease~**log**(heterotrophy.C),data=growth.y[growth.y$Prey=='HP'&growth.y$Fed=='Y',]); su

```
##
## Call:
```

```
## lm(formula = relincrease ~ log(heterotrophy.C), data = growth.y[growth.y$Prey ==
##     "HP" & growth.y$Fed == "Y", ])
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.75770 -0.36393 -0.07023  0.48471  0.89482
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)         3.3804     0.2635  12.828 4.06e-06 ***
## log(heterotrophy.C) -1.5767     0.8801  -1.791    0.116
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.6409 on 7 degrees of freedom
## Multiple R-squared:  0.3143, Adjusted R-squared:  0.2164
## F-statistic: 3.209 on 1 and 7 DF,  p-value: 0.1163
```

`plot(log(as.numeric(as.character(growth.y$heterotrophy.C))),growth.y$relincrease,pch=c(21,22,24)[as.fact`
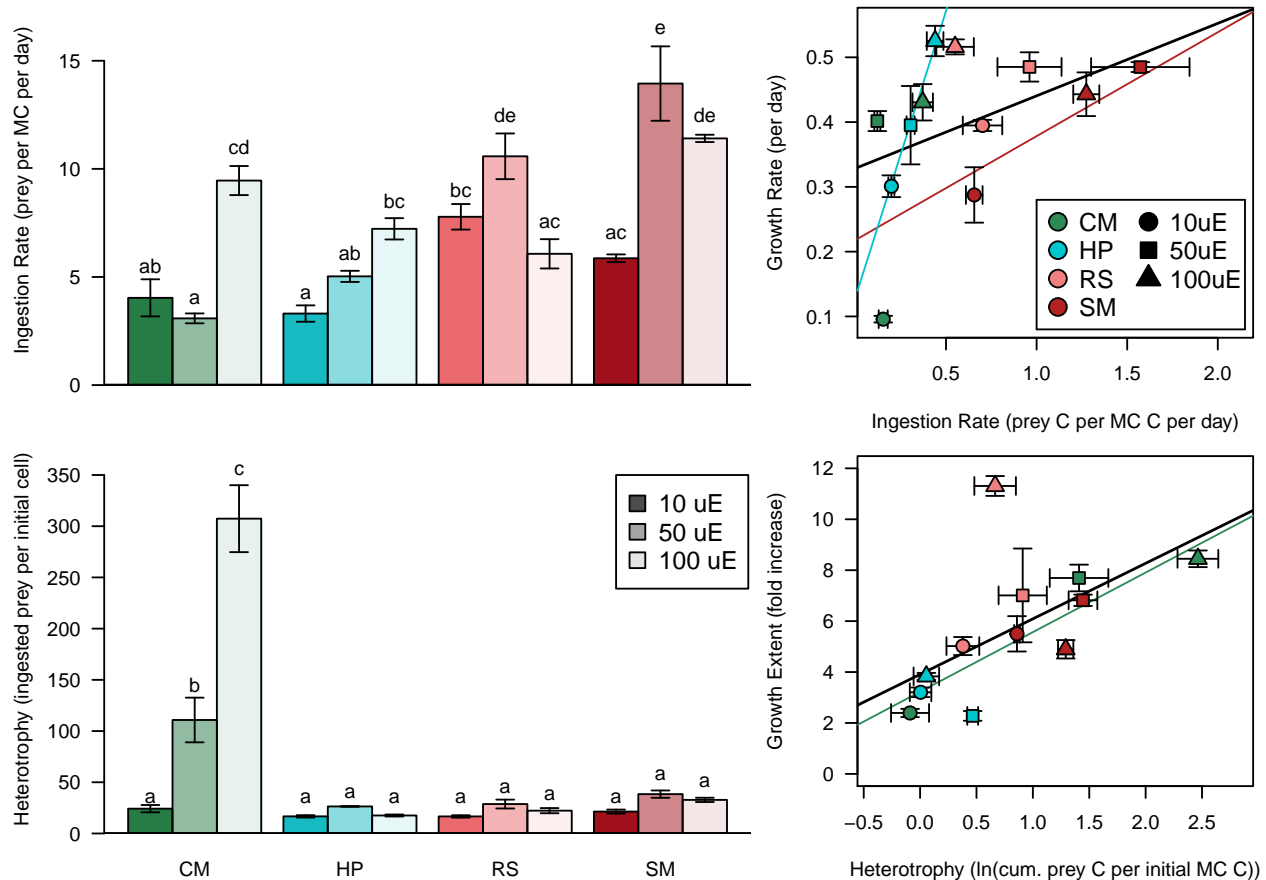
`#legend(1050,12.2,legend=c('CM','HP','RS','SM'),pch=21,pt.cex=ptcex,pt.bg=preycolvec,bty='n'); arrows(c`

Figure 5, revision 2: Heterotrophic contributions to growth, linear heterotrophy

```r
#layout(matrix(c(1,1,1,2,2,2,8,3,3,3,4,4,4,7,5,5,5,6,6,6,9),nrow=(6*3+3),ncol=1))
layout(matrix(c(1,1,1,2,2,3,3,3,4,4),nrow=2,ncol=5,byrow=TRUE))
xcoords <- c(1,2,3,4.5,5.5,6.5,8,9,10,11.5,12.5,13.5)
```

```r
# ingestion rate
par(mar=c(2,4,0.5,0.5))
bargraph.CI(Prey,ingest_2,group=Light,data=growth[growth$Fed=='Y',],legend=FALSE,x.leg=1,y.leg=15,ylim=
```

```r
par(mar=c(4,4,1,0.5))
```

```r
# SECOND PLOT: ingestion rate vs growth rate
# Revision: convert to per carbon
carbon$Prey.Rep <- paste(carbon$Prey,carbon$Rep,sep='.')
carbon$Sp.Rep <- paste(carbon$Species,carbon$Rep,sep='.')
growth$Prey.Rep <- paste(growth$Prey,growth$Rep,sep='.')
growth$MC.C <- carbon[carbon$Species=='MC',]$ngC_cell[match(growth$Prey.Rep,carbon[carbon$Species=='MC'
growth$prey.C <- carbon[carbon$Species!='MC',]$ngC_cell[match(growth$Prey.Rep,carbon[carbon$Species!='M
```

```r
growth$preyCperMCperday <- growth$ingest_2*growth$prey.C/growth$MC.C
growth$heterotrophy.C <- growth$PreyperMC*growth$prey.C/growth$MC.C
```

```r
lm.all <- lm(growth[growth$Fed=='Y',]$muMC~growth[growth$Fed=='Y',]$preyCperMCperday); summary(lm.all)
```

```
##
## Call:
## lm(formula = growth[growth$Fed == "Y", ]$muMC ~ growth[growth$Fed ==
##     "Y", ]$preyCperMCperday)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.25597 -0.06217  0.02526  0.07555  0.17508
##
## Coefficients:
##                                               Estimate Std. Error t value
## (Intercept)                                    0.32865    0.03136   10.48
## growth[growth$Fed == "Y", ]$preyCperMCperday   0.11187    0.04098    2.73
##                                               Pr(>|t|)
## (Intercept)                                    3.46e-12 ***
## growth[growth$Fed == "Y", ]$preyCperMCperday   0.00996 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.1141 on 34 degrees of freedom
## Multiple R-squared:  0.1798, Adjusted R-squared:  0.1557
## F-statistic: 7.454 on 1 and 34 DF,  p-value: 0.009955
```

```r
lm.RS <- lm(muMC~preyCperMCperday,data=growth[growth$Prey=='RS'&growth$Fed=='Y',]); summary(lm.RS) #n.s
```

```
##
## Call:
## lm(formula = muMC ~ preyCperMCperday, data = growth[growth$Prey ==
##     "RS" & growth$Fed == "Y", ])
```

```
##
## Residuals:
##       Min        1Q    Median        3Q       Max
## -0.085490 -0.059006  0.004134  0.052806  0.070208
##
## Coefficients:
##                 Estimate Std. Error t value Pr(>|t|)
## (Intercept)      0.45052    0.06457   6.977 0.000216 ***
## preyCperMCperday 0.02013    0.08278   0.243 0.814840
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.06314 on 7 degrees of freedom
## Multiple R-squared:  0.008377,   Adjusted R-squared:  -0.1333
## F-statistic: 0.05914 on 1 and 7 DF,  p-value: 0.8148
```

```r
lm.SM <- lm(muMC~preyCperMCperday,data=growth[growth$Prey=='SM'&growth$Fed=='Y',]); summary(lm.SM) #sig
```

```
##
## Call:
## lm(formula = muMC ~ preyCperMCperday, data = growth[growth$Prey ==
##     "SM" & growth$Fed == "Y", ])
##
## Residuals:
##       Min        1Q    Median        3Q       Max
## -0.089937 -0.058651 -0.009645  0.053621  0.085126
##
## Coefficients:
##                 Estimate Std. Error t value Pr(>|t|)
## (Intercept)      0.21793    0.06763   3.222   0.0146 *
## preyCperMCperday 0.16037    0.05410   2.964   0.0210 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.07253 on 7 degrees of freedom
## Multiple R-squared:  0.5566, Adjusted R-squared:  0.4932
## F-statistic: 8.786 on 1 and 7 DF,  p-value: 0.02098
```

```r
lm.CM <- lm(muMC~preyCperMCperday,data=growth[growth$Prey=='CM'&growth$Fed=='Y',]); summary(lm.CM) #n.s
```

```
##
## Call:
## lm(formula = muMC ~ preyCperMCperday, data = growth[growth$Prey ==
##     "CM" & growth$Fed == "Y", ])
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -0.2038 -0.1670  0.0300  0.1156  0.1690
##
## Coefficients:
##                 Estimate Std. Error t value Pr(>|t|)
## (Intercept)       0.1974     0.1066   1.852    0.106
## preyCperMCperday  0.5200     0.4302   1.209    0.266
##
## Residual standard error: 0.1585 on 7 degrees of freedom
```

```
## Multiple R-squared:  0.1727, Adjusted R-squared:  0.0545
## F-statistic: 1.461 on 1 and 7 DF,  p-value: 0.266

lm.HP <- lm(muMC~preyCperMCperday,data=growth[growth$Prey=='HP'&growth$Fed=='Y',]); summary(lm.HP) #sig

##
## Call:
## lm(formula = muMC ~ preyCperMCperday, data = growth[growth$Prey ==
##     "HP" & growth$Fed == "Y", ])
##
## Residuals:
##       Min        1Q    Median        3Q       Max
## -0.095104 -0.023532  0.002273  0.042511  0.052887
##
## Coefficients:
##                  Estimate Std. Error t value Pr(>|t|)
## (Intercept)       0.12936    0.05598   2.311  0.05412 .
## preyCperMCperday  0.88395    0.16847   5.247  0.00119 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.0546 on 7 degrees of freedom
## Multiple R-squared:  0.7973, Adjusted R-squared:  0.7683
## F-statistic: 27.53 on 1 and 7 DF,  p-value: 0.00119

plot(growth[growth$Fed=='Y',]$preyCperMCperday,growth[growth$Fed=='Y',]$muMC,las=1,pch=c(21,22,24)[as.f
C.summ <- summarySE(data=growth[growth$Fed=='Y',],measurevar='muMC',groupvars=c('Light','Prey')); I.summ

legend(1.5,0.29,legend=c('10uE','50uE','100uE'),pch=c(21,22,24),pt.cex=ptcex,pt.bg='black',col='black',l



# linear scale: prey per initial MC
par(mar=c(2,4,0.5,0.5))
bargraph.CI(Prey,(PreyperMC),group=Light,data=growth[growth$Fed=='Y',],legend=FALSE,err.width=0.05,names


# FOURTH PLOT: total ingestion vs growth extent

par(mar=c(4,4,1,0.5))
growth.y <- growth[growth$Fed=='Y',]
lm.all <- lm(growth.y$relincrease~(growth.y$heterotrophy.C)); summary(lm.all) #signif.; F-stat = 9.359,

##
## Call:
## lm(formula = growth.y$relincrease ~ (growth.y$heterotrophy.C))
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -3.1811 -1.6836 -0.5064  0.5715  6.4918
##
## Coefficients:
##                        Estimate Std. Error t value Pr(>|t|)
## (Intercept)              4.4469     0.5822   7.638 7.08e-09 ***
## growth.y$heterotrophy.C  0.4003     0.1309   3.059  0.00431 **
```

```
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2.483 on 34 degrees of freedom
## Multiple R-squared:  0.2158, Adjusted R-squared:  0.1928
## F-statistic: 9.359 on 1 and 34 DF,  p-value: 0.004308
```

```r
lm.RS.f <- lm(relincrease~(heterotrophy.C),data=growth.y[growth.y$Prey=='RS'&growth.y$Fed=='Y',]); summa
```

```
##
## Call:
## lm(formula = relincrease ~ (heterotrophy.C), data = growth.y[growth.y$Prey ==
##     "RS" & growth.y$Fed == "Y", ])
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -2.6741 -2.3507 -0.6151  2.8925  4.1745
##
## Coefficients:
##                Estimate Std. Error t value Pr(>|t|)
## (Intercept)       3.549      2.954   1.201    0.269
## heterotrophy.C    2.079      1.366   1.522    0.172
##
## Residual standard error: 3.002 on 7 degrees of freedom
## Multiple R-squared:  0.2487, Adjusted R-squared:  0.1413
## F-statistic: 2.317 on 1 and 7 DF,  p-value: 0.1718
```

```r
lm.SM.f <- lm(relincrease~(heterotrophy.C),data=growth.y[growth.y$Prey=='SM'&growth.y$Fed=='Y',]); summa
```

```
##
## Call:
## lm(formula = relincrease ~ (heterotrophy.C), data = growth.y[growth.y$Prey ==
##     "SM" & growth.y$Fed == "Y", ])
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -1.5751 -0.9955  0.2146  0.6647  1.3919
##
## Coefficients:
##                Estimate Std. Error t value Pr(>|t|)
## (Intercept)      4.3340     1.3600   3.187   0.0153 *
## heterotrophy.C   0.4079     0.3806   1.072   0.3194
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.095 on 7 degrees of freedom
## Multiple R-squared:  0.1409, Adjusted R-squared:  0.01821
## F-statistic: 1.148 on 1 and 7 DF,  p-value: 0.3194
```

```r
lm.CM.f <- lm(relincrease~(heterotrophy.C),data=growth.y[growth.y$Prey=='CM'&growth.y$Fed=='Y',]); summa
```

```
##
## Call:
## lm(formula = relincrease ~ (heterotrophy.C), data = growth.y[growth.y$Prey ==
##     "CM" & growth.y$Fed == "Y", ])
##
```

```
## Residuals:
##     Min      1Q  Median      3Q     Max
## -1.9497 -1.8459  0.1185  1.1614  2.7263
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)     3.8178     1.0203   3.742  0.00725 **
## heterotrophy.C  0.4059     0.1316   3.085  0.01768 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2.025 on 7 degrees of freedom
## Multiple R-squared:  0.5763, Adjusted R-squared:  0.5157
## F-statistic:  9.52 on 1 and 7 DF,  p-value: 0.01768
```

```r
lm.HP.f <- lm(relincrease~(heterotrophy.C),data=growth.y[growth.y$Prey=='HP'&growth.y$Fed=='Y',]); summa
```

```
##
## Call:
## lm(formula = relincrease ~ (heterotrophy.C), data = growth.y[growth.y$Prey ==
##     "HP" & growth.y$Fed == "Y", ])
##
## Residuals:
##       Min       1Q   Median       3Q      Max
## -0.70989 -0.39720 -0.06457  0.43601  0.85154
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)     4.8143     0.8681   5.546 0.000864 ***
## heterotrophy.C -1.3936     0.6874  -2.027 0.082224 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.6143 on 7 degrees of freedom
## Multiple R-squared:  0.37,  Adjusted R-squared:   0.28
## F-statistic:  4.11 on 1 and 7 DF,  p-value: 0.08222
```

```r
plot((as.numeric(as.character(growth.y$heterotrophy.C))),growth.y$relincrease,pch=c(21,22,24)[as.factor
```
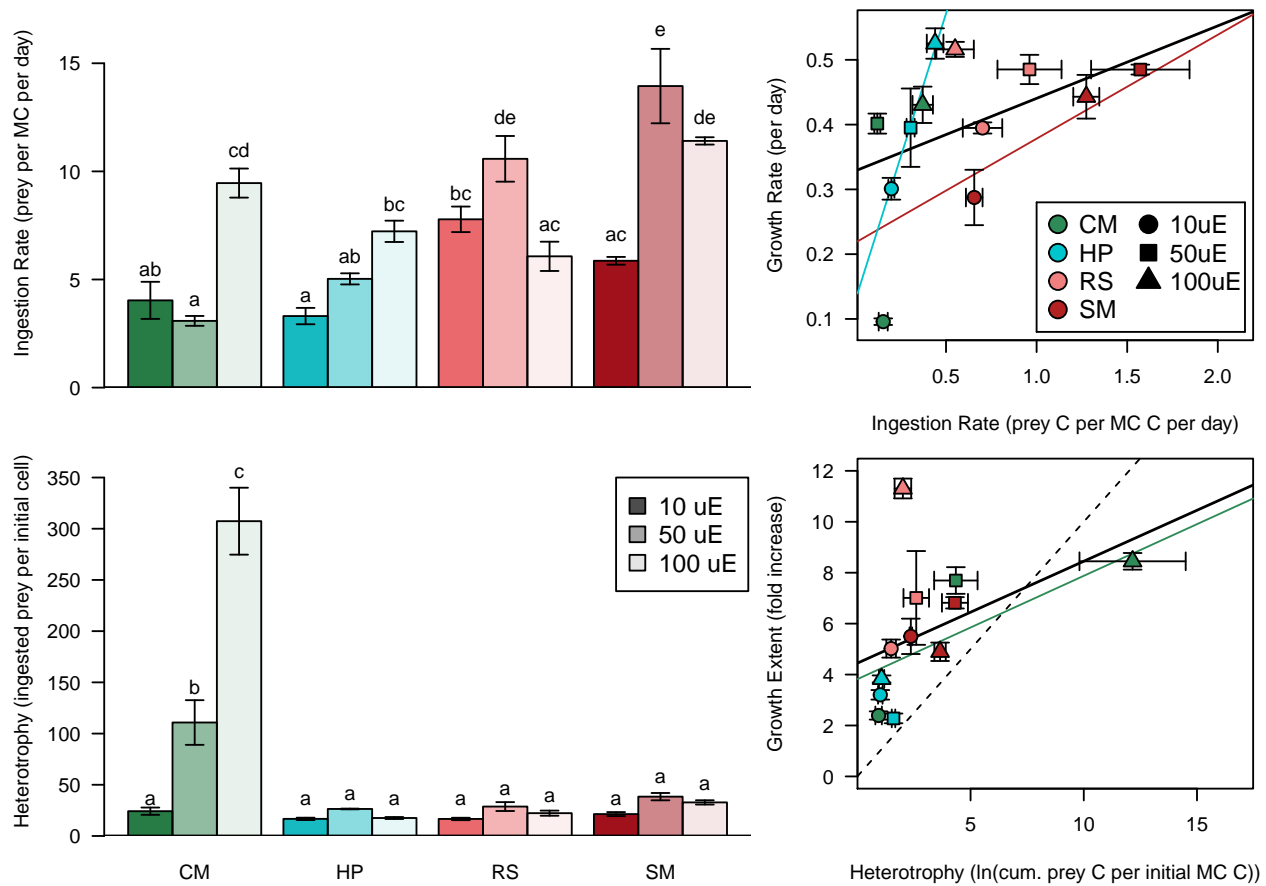
Figure 6: Photosynthetic contributions to growth

```
layout(matrix(c(8,1,2,3,4,rep(7,3),9,5,5,5,5,rep(7,3),10,6,6,6,6,rep(7,3)),nrow=3,ncol=8,byrow=TRUE));


growth$C.fixed3 <- growth$C.fixed2/1000 # convert from pg to ng
growth$C.per.prey <- growth$C.fixed2/growth$TotPreyCons


xcoords <- c(1.2,3.4,5.6)
xcoords2 <- c(.7,1.7,2.9,3.9,5.1,6.1)
#quartz(height=3.5,width=7.5)
par(mar=c(1,1,0.5,0.5))
#layout(matrix(c(7,1,1,1,2,2,2,3,3,3,4,4,4,rep(6,6),8,rep(5,3*4),rep(6,6)),nrow=2,ncol=19,byrow=TRUE))


# Row 1: Photosynthate
ymax <- 50; ymin <- 0; bargraph.CI(Light,C.fixed3,group=Fed,data=growth[growth$Prey=='CM',],las=1,legend


bargraph.CI(Light,C.fixed3,group=Fed,data=growth[growth$Prey=='HP',],las=1,legend=FALSE,leg.lab=c('Starv


bargraph.CI(Light,C.fixed3,group=Fed,data=growth[growth$Prey=='RS',],las=1,legend=FALSE,ylim=c(ymin,ymax
```

```r
bargraph.CI(Light,C.fixed3,group=Fed,data=growth[growth$Prey=='SM',],las=1,legend=TRUE,leg.lab=c('Starve

# Second row: fold difference
xcoords <- c(1,2,3,4.5,5.5,6.5,8,9,10,11.5,12.5,13.5)

bargraph.CI(Prey,C.fixed2/abs(deltaCfixed-C.fixed2),group=Light,data=growth[growth$Fed=='Y',],legend=FAI

#TukeyHSD(aov(C.fixed2/abs(deltaCfixed-C.fixed2)~as.factor(Light)*Prey,data=growth[growth$Fed=='Y',]))

# Third row: Carbon fixed per prey ingested
bargraph.CI(Prey,C.per.prey,group=Light,data=growth[growth$Fed=='Y',],legend=FALSE,err.width=0.05,las=3

#TukeyHSD(aov(C.per.prey~as.factor(Light)*Prey,data=growth[growth$Fed=='Y',]))

# FOURTH PLOT: total photosynthate vs growth extent
par(mar=c(4,5,.5,0.5))

lm.all <- lm(growth$relincrease~growth$C.fixed3); summary(lm.all) #signif.; F-stat = 363.6, p-val = < 2
```

```
## 
## Call:
## lm(formula = growth$relincrease ~ growth$C.fixed3)
## 
## Residuals:
##     Min      1Q  Median      3Q     Max
## -1.7400 -0.7034 -0.2552  0.6855  3.4925
## 
## Coefficients:
##                 Estimate Std. Error t value Pr(>|t|)
## (Intercept)      1.46273    0.18230   8.024 1.65e-11 ***
## growth$C.fixed3  0.19933    0.01041  19.152  < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 1.132 on 70 degrees of freedom
## Multiple R-squared:  0.8397, Adjusted R-squared:  0.8374
## F-statistic: 366.8 on 1 and 70 DF,  p-value: < 2.2e-16
```

```r
lm.RS.f <- lm(relincrease~C.fixed3,data=growth[growth$Prey=='RS'&growth$Fed=='Y',]); summary(lm.RS.f) #:
```

```
## 
## Call:
## lm(formula = relincrease ~ C.fixed3, data = growth[growth$Prey ==
##     "RS" & growth$Fed == "Y", ])
## 
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.58623 -0.24859  0.08797  0.55830  1.53320
## 
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  2.59415    0.75984   3.414 0.011225 *
```

```
## C.fixed3     0.20795    0.02661    7.814 0.000106 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.111 on 7 degrees of freedom
## Multiple R-squared:  0.8972, Adjusted R-squared:  0.8825
## F-statistic: 61.06 on 1 and 7 DF,  p-value: 0.0001059
```

```r
lm.RS.n <- lm(relincrease~C.fixed3,data=growth[growth$Prey=='RS'&growth$Fed=='N',]); summary(lm.RS.n) #
```

```
##
## Call:
## lm(formula = relincrease ~ C.fixed3, data = growth[growth$Prey ==
##     "RS" & growth$Fed == "N", ])
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.60262 -0.35354 -0.06898  0.27792  0.72256
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  1.19688    0.25227   4.744   0.0021 **
## C.fixed3     0.17056    0.01769   9.640 2.72e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.4955 on 7 degrees of freedom
## Multiple R-squared:  0.9299, Adjusted R-squared:  0.9199
## F-statistic: 92.92 on 1 and 7 DF,  p-value: 2.724e-05
```

```r
lm.SM.f <- lm(relincrease~C.fixed3,data=growth[growth$Prey=='SM'&growth$Fed=='Y',]); summary(lm.SM.f) #
```

```
##
## Call:
## lm(formula = relincrease ~ C.fixed3, data = growth[growth$Prey ==
##     "SM" & growth$Fed == "Y", ])
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.40307 -1.20669  0.05384  0.96935  1.36544
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  5.36265    0.95182   5.634 0.000787 ***
## C.fixed3     0.02059    0.04768   0.432 0.678818
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.166 on 7 degrees of freedom
## Multiple R-squared:  0.02595,   Adjusted R-squared:  -0.1132
## F-statistic: 0.1865 on 1 and 7 DF,  p-value: 0.6788
```

```r
lm.SM.n <- lm(relincrease~C.fixed3,data=growth[growth$Prey=='SM'&growth$Fed=='N',]); summary(lm.SM.n) #
```

```
##
## Call:
```

```
## lm(formula = relincrease ~ C.fixed3, data = growth[growth$Prey ==
##     "SM" & growth$Fed == "N", ])
##
## Residuals:
##      Min      1Q   Median      3Q      Max
## -0.62041 -0.35385 -0.01644  0.24170  0.87923
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  1.70731    0.31843   5.362  0.00105 **
## C.fixed3     0.04822    0.04356   1.107  0.30491
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.5083 on 7 degrees of freedom
## Multiple R-squared:  0.149,  Adjusted R-squared:  0.02739
## F-statistic: 1.225 on 1 and 7 DF,  p-value: 0.3049
```

```r
lm.CM.f <- lm(relincrease~C.fixed3,data=growth[growth$Prey=='CM'&growth$Fed=='Y',]); summary(lm.CM.f) #
```

```
##
## Call:
## lm(formula = relincrease ~ C.fixed3, data = growth[growth$Prey ==
##     "CM" & growth$Fed == "Y", ])
##
## Residuals:
##       Min       1Q   Median       3Q      Max
## -0.55407 -0.29453  0.04931  0.17498  0.76372
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) 2.245605   0.241095   9.314 3.41e-05 ***
## C.fixed3    0.156242   0.007878  19.832 2.07e-07 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.4114 on 7 degrees of freedom
## Multiple R-squared:  0.9825, Adjusted R-squared:   0.98
## F-statistic: 393.3 on 1 and 7 DF,  p-value: 2.072e-07
```

```r
lm.CM.n <- lm(relincrease~C.fixed3,data=growth[growth$Prey=='CM'&growth$Fed=='N',]); summary(lm.CM.n) #
```

```
##
## Call:
## lm(formula = relincrease ~ C.fixed3, data = growth[growth$Prey ==
##     "CM" & growth$Fed == "N", ])
##
## Residuals:
##      Min      1Q  Median      3Q      Max
## -0.5348 -0.5008  0.1913  0.2208  0.5839
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)   0.9822     0.3281   2.994   0.0201 *
## C.fixed3      0.2358     0.1594   1.480   0.1825
```

```
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.4506 on 7 degrees of freedom
## Multiple R-squared:  0.2383, Adjusted R-squared:  0.1294
## F-statistic:  2.19 on 1 and 7 DF,  p-value: 0.1825
```

```r
lm.HP.f <- lm(relincrease~C.fixed3,data=growth[growth$Prey=='HP'&growth$Fed=='Y',]); summary(lm.HP.f) #
```

```
##
## Call:
## lm(formula = relincrease ~ C.fixed3, data = growth[growth$Prey ==
##     "HP" & growth$Fed == "Y", ])
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.86859 -0.12767 -0.00792  0.28699  0.74476
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  1.65699    0.46685   3.549  0.00935 **
## C.fixed3     0.26614    0.08058   3.303  0.01307 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.4839 on 7 degrees of freedom
## Multiple R-squared:  0.6091, Adjusted R-squared:  0.5533
## F-statistic: 10.91 on 1 and 7 DF,  p-value: 0.01307
```

```r
lm.HP.n <- lm(relincrease~C.fixed3,data=growth[growth$Prey=='HP'&growth$Fed=='N',]); summary(lm.HP.n) #
```

```
##
## Call:
## lm(formula = relincrease ~ C.fixed3, data = growth[growth$Prey ==
##     "HP" & growth$Fed == "N", ])
##
## Residuals:
##        Min        1Q    Median        3Q       Max
## -0.225199 -0.113317  0.005071  0.097854  0.232258
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)   1.1518     0.1637   7.035 0.000205 ***
## C.fixed3      0.1117     0.0533   2.095 0.074397 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.1625 on 7 degrees of freedom
## Multiple R-squared:  0.3854, Adjusted R-squared:  0.2976
## F-statistic:  4.39 on 1 and 7 DF,  p-value: 0.0744
```

```r
plot(growth$C.fixed2/1000,growth$relincrease,pch=c(21,22)[growth$Fed],bg=preycolvec[growth$Prey],las=1,
```

```
## Warning in arrows(C.summ[, 5]/1000, I.summ[, 5] + I.summ$se, C.summ[, 5]/
## 1000, : zero-length arrow is of indeterminate angle and so skipped
```

```
TukeyHSD(aov(C.fixed3~Fed*as.factor(Light),data=growth[growth$Prey=='SM',]))
```

```
##   Tukey multiple comparisons of means
##     95% family-wise confidence level
##
## Fit: aov(formula = C.fixed3 ~ Fed * as.factor(Light), data = growth[growth$Prey == "SM", ])
##
## $Fed
##          diff      lwr      upr p adj
## Y-N 12.03204 9.951656 14.11241     0
##
## $`as.factor(Light)`
##              diff        lwr       upr     p adj
## 50-10    9.852058  6.7322214 12.971895 0.0000061
## 100-10  13.429425 10.3095887 16.549262 0.0000002
## 100-50   3.577367  0.4575305  6.697204 0.0249375
##
## $`Fed:as.factor(Light)`
##                    diff        lwr        upr     p adj
## Y:10-N:10     5.2820940 -0.2728926 10.837081 0.0658299
## N:50-N:10     4.3741001 -1.1808865  9.929087 0.1592640
## Y:50-N:10    20.6121102 15.0571236 26.167097 0.0000004
## N:100-N:10    8.7824715  3.2274850 14.337458 0.0019704
## Y:100-N:10   23.3584733 17.8034867 28.913460 0.0000001
## N:50-Y:10    -0.9079939 -6.4629805  4.646993 0.9926408
## Y:50-Y:10    15.3300162  9.7750296 20.885003 0.0000094
## N:100-Y:10    3.5003776 -2.0546090  9.055364 0.3407546
## Y:100-Y:10   18.0763793 12.5213927 23.631366 0.0000016
## Y:50-N:50    16.2380101 10.6830236 21.792997 0.0000051
## N:100-N:50    4.4083715 -1.1466151  9.963358 0.1542413
## Y:100-N:50   18.9843732 13.4293867 24.539360 0.0000009
## N:100-Y:50  -11.8296386 -17.3846252 -6.274652 0.0001313
## Y:100-Y:50    2.7463631 -2.8086235  8.301350 0.5786171
## Y:100-N:100  14.5760018  9.0210152 20.130988 0.0000160
```
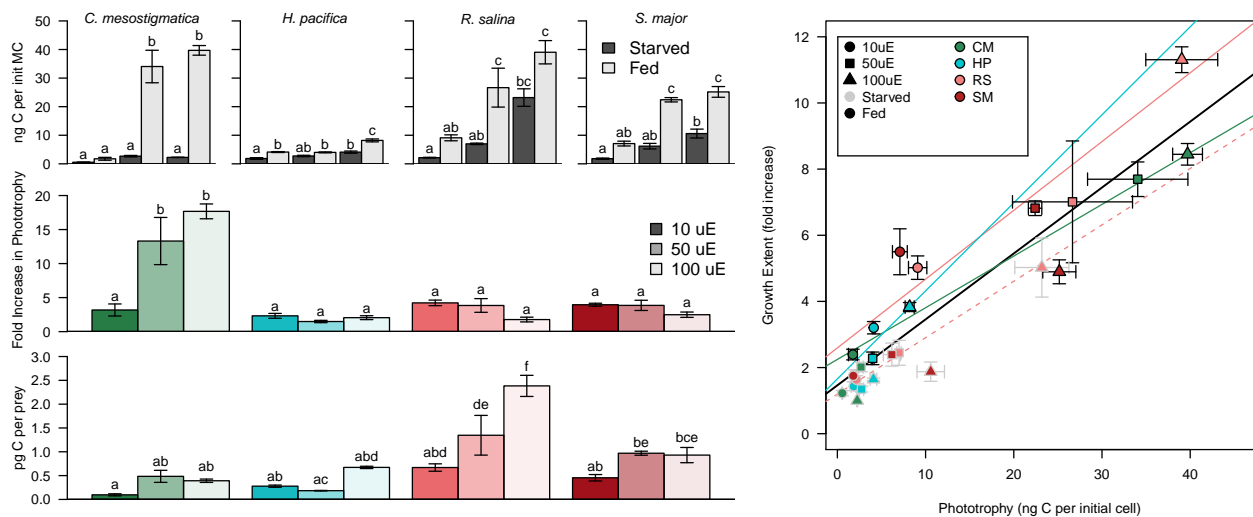
Figure 6, Revision: Photosynthetic contributions to growth

```r
layout(matrix(c(8,1,2,3,4,rep(7,3),9,5,5,5,5,rep(7,3),10,6,6,6,6,rep(7,3)),nrow=3,ncol=8,byrow=TRUE));


growth$C.fixed3 <- growth$C.fixed2/1000 # convert from pg to ng
growth$C.per.prey <- growth$C.fixed2/growth$TotPreyCons
growth$C.fixed.perMC.C <- growth$C.fixed3/growth$MC.C # convert from per MC cell to per MC ng C


xcoords <- c(1.2,3.4,5.6)
xcoords2 <- c(.7,1.7,2.9,3.9,5.1,6.1)
#quartz(height=3.5,width=7.5)
par(mar=c(1,1,0.5,0.5))
#layout(matrix(c(7,1,1,1,2,2,2,3,3,3,4,4,4,rep(6,6),8,rep(5,3*4),rep(6,6)),nrow=2,ncol=19,byrow=TRUE))

# Row 1: Photosynthate
ymax <- 50; ymin <- 0; bargraph.CI(Light,C.fixed3,group=Fed,data=growth[growth$Prey=='CM',],las=1,legen


bargraph.CI(Light,C.fixed3,group=Fed,data=growth[growth$Prey=='HP',],las=1,legend=FALSE,leg.lab=c('Starv

bargraph.CI(Light,C.fixed3,group=Fed,data=growth[growth$Prey=='RS',],las=1,legend=FALSE,ylim=c(ymin,yma

bargraph.CI(Light,C.fixed3,group=Fed,data=growth[growth$Prey=='SM',],las=1,legend=TRUE,leg.lab=c('Starv



# Second row: fold difference
xcoords <- c(1,2,3,4.5,5.5,6.5,8,9,10,11.5,12.5,13.5)

bargraph.CI(Prey,C.fixed2/abs(deltaCfixed-C.fixed2),group=Light,data=growth[growth$Fed=='Y',],legend=FA

#TukeyHSD(aov(C.fixed2/abs(deltaCfixed-C.fixed2)~as.factor(Light)*Prey,data=growth[growth$Fed=='Y',]))

# Third row: Carbon fixed per prey ingested
bargraph.CI(Prey,C.per.prey,group=Light,data=growth[growth$Fed=='Y',],legend=FALSE,err.width=0.05,las=3

#TukeyHSD(aov(C.per.prey~as.factor(Light)*Prey,data=growth[growth$Fed=='Y',]))

# FOURTH PLOT: total photosynthate vs growth extent
par(mar=c(4,5,.5,0.5))

lm.all <- lm(growth$relincrease~growth$C.fixed.perMC.C); summary(lm.all) #signif.; F-stat = 310.2, p-va

##
## Call:
## lm(formula = growth$relincrease ~ growth$C.fixed.perMC.C)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -2.6053 -0.7915 -0.0842  0.5028  3.4804
##
## Coefficients:
```

```
##                        Estimate Std. Error t value Pr(>|t|)
## (Intercept)            1.471040    0.196403    7.49 1.58e-10 ***
## growth$C.fixed.perMC.C 0.144306    0.008194   17.61  < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.214 on 70 degrees of freedom
## Multiple R-squared:  0.8159, Adjusted R-squared:  0.8132
## F-statistic: 310.2 on 1 and 70 DF,  p-value: < 2.2e-16
```

```r
lm.RS.f <- lm(relincrease~C.fixed.perMC.C,data=growth[growth$Prey=='RS'&growth$Fed=='Y',]); summary(lm.
```

```
##
## Call:
## lm(formula = relincrease ~ C.fixed.perMC.C, data = growth[growth$Prey ==
##     "RS" & growth$Fed == "Y", ])
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -1.7067 -0.5820 -0.3065  0.5846  2.8392
##
## Coefficients:
##                 Estimate Std. Error t value Pr(>|t|)
## (Intercept)      3.29289    0.88856   3.706 0.007596 **
## C.fixed.perMC.C  0.11449    0.01926   5.946 0.000572 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.408 on 7 degrees of freedom
## Multiple R-squared:  0.8347, Adjusted R-squared:  0.8111
## F-statistic: 35.36 on 1 and 7 DF,  p-value: 0.0005724
```

```r
lm.RS.n <- lm(relincrease~C.fixed.perMC.C,data=growth[growth$Prey=='RS'&growth$Fed=='N',]); summary(lm.
```

```
##
## Call:
## lm(formula = relincrease ~ C.fixed.perMC.C, data = growth[growth$Prey ==
##     "RS" & growth$Fed == "N", ])
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -1.0589 -0.4481 -0.1226  0.1940  1.5581
##
## Coefficients:
##                 Estimate Std. Error t value Pr(>|t|)
## (Intercept)      1.27520    0.44228   2.883  0.02354 *
## C.fixed.perMC.C  0.10831    0.02089   5.185  0.00127 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.8509 on 7 degrees of freedom
## Multiple R-squared:  0.7934, Adjusted R-squared:  0.7639
## F-statistic: 26.89 on 1 and 7 DF,  p-value: 0.001273
```

```r
lm.SM.f <- lm(relincrease~C.fixed.perMC.C,data=growth[growth$Prey=='SM'&growth$Fed=='Y',]); summary(lm.S
```

```
## 
## Call:
## lm(formula = relincrease ~ C.fixed.perMC.C, data = growth[growth$Prey ==
##     "SM" & growth$Fed == "Y", ])
## 
## Residuals:
##      Min      1Q  Median      3Q     Max
## -1.45815 -1.12985  0.05021  1.03924  1.31004
## 
## Coefficients:
##                 Estimate Std. Error t value Pr(>|t|)
## (Intercept)      5.40066    0.90738   5.952 0.000569 ***
## C.fixed.perMC.C  0.01303    0.03166   0.411 0.693081
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 1.168 on 7 degrees of freedom
## Multiple R-squared:  0.02361,    Adjusted R-squared:  -0.1159
## F-statistic: 0.1693 on 1 and 7 DF,  p-value: 0.6931
```

```r
lm.SM.n <- lm(relincrease~C.fixed.perMC.C,data=growth[growth$Prey=='SM'&growth$Fed=='N',]); summary(lm.S
```

```
## 
## Call:
## lm(formula = relincrease ~ C.fixed.perMC.C, data = growth[growth$Prey ==
##     "SM" & growth$Fed == "N", ])
## 
## Residuals:
##      Min      1Q  Median      3Q     Max
## -0.64964 -0.41897 -0.05582  0.23975  0.89258
## 
## Coefficients:
##                 Estimate Std. Error t value Pr(>|t|)
## (Intercept)      1.77948    0.34584   5.145  0.00133 **
## C.fixed.perMC.C  0.02631    0.03458   0.761  0.47162
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 0.5295 on 7 degrees of freedom
## Multiple R-squared:  0.07637,    Adjusted R-squared:  -0.05557
## F-statistic: 0.5788 on 1 and 7 DF,  p-value: 0.4716
```

```r
lm.CM.f <- lm(relincrease~C.fixed.perMC.C,data=growth[growth$Prey=='CM'&growth$Fed=='Y',]); summary(lm.C
```

```
## 
## Call:
## lm(formula = relincrease ~ C.fixed.perMC.C, data = growth[growth$Prey ==
##     "CM" & growth$Fed == "Y", ])
## 
## Residuals:
##      Min      1Q  Median      3Q     Max
## -0.76078 -0.38033 -0.08572  0.36568  0.64725
## 
## Coefficients:
##                 Estimate Std. Error t value Pr(>|t|)
```

```
## (Intercept)     2.329967    0.296329    7.863 0.000102 ***
## C.fixed.perMC.C 0.151643    0.009551   15.877 9.54e-07 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.5114 on 7 degrees of freedom
## Multiple R-squared:  0.973,  Adjusted R-squared:  0.9691
## F-statistic: 252.1 on 1 and 7 DF,  p-value: 9.538e-07
```

```r
lm.CM.n <- lm(relincrease~C.fixed.perMC.C,data=growth[growth$Prey=='CM'&growth$Fed=='N',]); summary(lm.C
```

```
##
## Call:
## lm(formula = relincrease ~ C.fixed.perMC.C, data = growth[growth$Prey ==
##     "CM" & growth$Fed == "N", ])
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -0.5195 -0.4890  0.1743  0.2045  0.6383
##
## Coefficients:
##                 Estimate Std. Error t value Pr(>|t|)
## (Intercept)       0.9986     0.3304   3.022   0.0193 *
## C.fixed.perMC.C   0.2260     0.1598   1.415   0.2000
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.4553 on 7 degrees of freedom
## Multiple R-squared:  0.2224, Adjusted R-squared:  0.1113
## F-statistic: 2.002 on 1 and 7 DF,  p-value: 0.2
```

```r
lm.HP.f <- lm(relincrease~C.fixed.perMC.C,data=growth[growth$Prey=='HP'&growth$Fed=='Y',]); summary(lm.
```
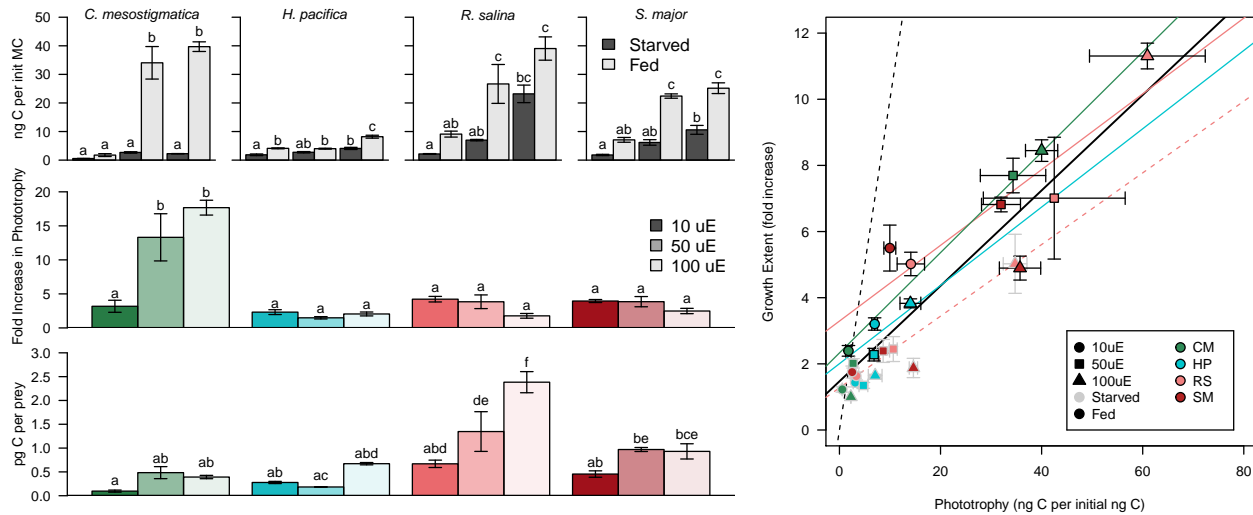
```
##
## Call:
## lm(formula = relincrease ~ C.fixed.perMC.C, data = growth[growth$Prey ==
##     "HP" & growth$Fed == "Y", ])
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.13493 -0.16503  0.01446  0.30774  0.76814
##
## Coefficients:
##                 Estimate Std. Error t value Pr(>|t|)
## (Intercept)      2.00481    0.49814   4.025  0.00503 **
## C.fixed.perMC.C  0.11838    0.04953   2.390  0.04816 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.5743 on 7 degrees of freedom
## Multiple R-squared:  0.4494, Adjusted R-squared:  0.3707
## F-statistic: 5.713 on 1 and 7 DF,  p-value: 0.04816
```

```r
lm.HP.n <- lm(relincrease~C.fixed.perMC.C,data=growth[growth$Prey=='HP'&growth$Fed=='N',]); summary(lm.
```

```
##
```

```
## Call:
## lm(formula = relincrease ~ C.fixed.perMC.C, data = growth[growth$Prey ==
##     "HP" & growth$Fed == "N", ])
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -0.2453 -0.1470  0.0246  0.1520  0.1974
##
## Coefficients:
##                 Estimate Std. Error t value Pr(>|t|)
## (Intercept)      1.29104    0.15938   8.100 8.42e-05 ***
## C.fixed.perMC.C  0.03706    0.02946   1.258    0.249
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.1872 on 7 degrees of freedom
## Multiple R-squared:  0.1844, Adjusted R-squared:  0.06786
## F-statistic: 1.582 on 1 and 7 DF,  p-value: 0.2488
```

```
plot(growth$C.fixed.perMC.C,growth$relincrease,pch=c(21,22)[growth$Fed],bg=preycolvec[growth$Prey],las=
```

```
## Warning in arrows(C.summ[, 5], I.summ[, 5] + I.summ$se, C.summ[, 5],
## I.summ[, : zero-length arrow is of indeterminate angle and so skipped
```

```
TukeyHSD(aov(C.fixed3~Fed*as.factor(Light),data=growth[growth$Prey=='SM',]))
```

```
##   Tukey multiple comparisons of means
##     95% family-wise confidence level
##
## Fit: aov(formula = C.fixed3 ~ Fed * as.factor(Light), data = growth[growth$Prey == "SM", ])
##
## $Fed
##          diff      lwr      upr p adj
## Y-N 12.03204 9.951656 14.11241     0
##
## $`as.factor(Light)`
##             diff        lwr       upr     p adj
## 50-10   9.852058  6.7322214 12.971895 0.0000061
## 100-10 13.429425 10.3095887 16.549262 0.0000002
## 100-50  3.577367  0.4575305  6.697204 0.0249375
##
## $`Fed:as.factor(Light)`
##                    diff        lwr       upr     p adj
## Y:10-N:10     5.2820940 -0.2728926 10.837081 0.0658299
## N:50-N:10     4.3741001 -1.1808865  9.929087 0.1592640
## Y:50-N:10    20.6121102 15.0571236 26.167097 0.0000004
## N:100-N:10    8.7824715  3.2274850 14.337458 0.0019704
## Y:100-N:10   23.3584733 17.8034867 28.913460 0.0000001
## N:50-Y:10    -0.9079939 -6.4629805  4.646993 0.9926408
## Y:50-Y:10    15.3300162  9.7750296 20.885003 0.0000094
## N:100-Y:10    3.5003776 -2.0546090  9.055364 0.3407546
## Y:100-Y:10   18.0763793 12.5213927 23.631366 0.0000016
## Y:50-N:50    16.2380101 10.6830236 21.792997 0.0000051
## N:100-N:50    4.4083715 -1.1466151  9.963358 0.1542413
## Y:100-N:50   18.9843732 13.4293867 24.539360 0.0000009
```

```
## N:100-Y:50   -11.8296386 -17.3846252  -6.274652 0.0001313
## Y:100-Y:50     2.7463631  -2.8086235   8.301350 0.5786171
## Y:100-N:100   14.5760018   9.0210152  20.130988 0.0000160
```


Supplementary Figures, Revision: Timeseries of cells and pigments

```r
# Choose the data columns to use, their names, and their maxima
#datcols <- c(8,9,30,dim(dat)[2]-2,dim(dat)[2]-1)
datcols <- c(which(names(dat)=='MC_cellspmL'),which(names(dat)=='Prey_cellspmL'),which(names(dat)=='Plas
ylabstrs <- c('MC (cells/mL)','Prey (cells/mL)','Plastids (per MC cell)','MC chl (pg/cell)','MC chl (pg,
ymax <- c(10000,25000,30,55,85,100)

# We will partition data by light level
lightvec <- c(10,50,100)
titlestr <- paste(as.character(lightvec),'uE'); titlestr <- rbind(titlestr,c(rep('',3)),c(rep('',3)),c(1

# Iterate over different prey types
preyvec <- c('CM','HP','RS','SM')
preycolvec <- c(CMcol,HPcol,RScol,SMcol)

# Step 1: choose your prey type & subset data

for(k in 1:length(preyvec)){

# Step 1: Choose the prey and subset data accordingly
preychoice <- preyvec[k]
dat.hold2 <- dat[dat$Prey==preychoice,]


par(mar=c(1,4,1,0.1),mfcol=c(length(datcols),length(lightvec)))
# Note that we've used the argument "mfcol" instead of "mfrow." This ensures that the subsequent mega-p

for(j in 1:length(lightvec)){

# Step 2: Subset the data again for appropriate light level
dat.hold <- dat.hold2[dat.hold2$Light==lightvec[j],]
```

```r
# Step 3: Create summary stats.
summ.MC<-summarySE(data=dat.hold,measurevar="MC_cellspmL",groupvars=c("ExptDay",'Fed'),na.rm=TRUE)
summ.prey<-summarySE(data=dat.hold,measurevar="Prey_cellspmL",groupvars=c("ExptDay",'Fed'),na.rm=TRUE)
summ.chl<-summarySE(data=dat.hold,measurevar="chl_p_cell",groupvars=c("ExptDay",'Fed'),na.rm=TRUE)
summ.chl.p.mL <- summarySE(data=dat.hold,measurevar='chl_p_mL',groupvars=c("ExptDay",'Fed'),na.rm=TRUE)
summ.chl.p.C <- summarySE(data=dat.hold,measurevar='ChlperC',groupvars=c("ExptDay",'Fed'),na.rm=TRUE)
summ.Plastids<-summarySE(data=dat.hold,measurevar="PlastidCount",groupvars=c("ExptDay",'Fed'),na.rm=TRUE

# Step 4: Make all the plots
for(i in 1:length(datcols)){

# Create axes using raw data
plot(dat.hold$ExptDay, dat.hold[,datcols[i]], type='n', las=1, xlab='', main=titlestr[i,j],ylim=c(0,ymax

if(i == 1){ summ.use <- summ.MC }; if(i == 2){ summ.use <- summ.prey }; if(i == 4){ summ.use <- summ.chl

# Plot lines connecting means
lines(summ.use[summ.use$Fed=='N',]$ExptDay,summ.use[summ.use$Fed=='N',][,4],col= Starvedcol); lines(summ

# Plot std error
summ.use.Y <- summ.use[summ.use$Fed=="Y",]; summ.use.N <- summ.use[summ.use$Fed=="N",]
arrows(summ.use.Y$ExptDay,summ.use.Y[,4]+summ.use.Y$se,summ.use.Y$ExptDay,summ.use.Y[,4]-summ.use.Y$se,

# Plot means
points(summ.use$ExptDay,summ.use[,4],pch=22,col=c(Starvedcol,Fedcol)[summ.use$Fed],bg=c(Starvedcol,Fedc

}}
}
```
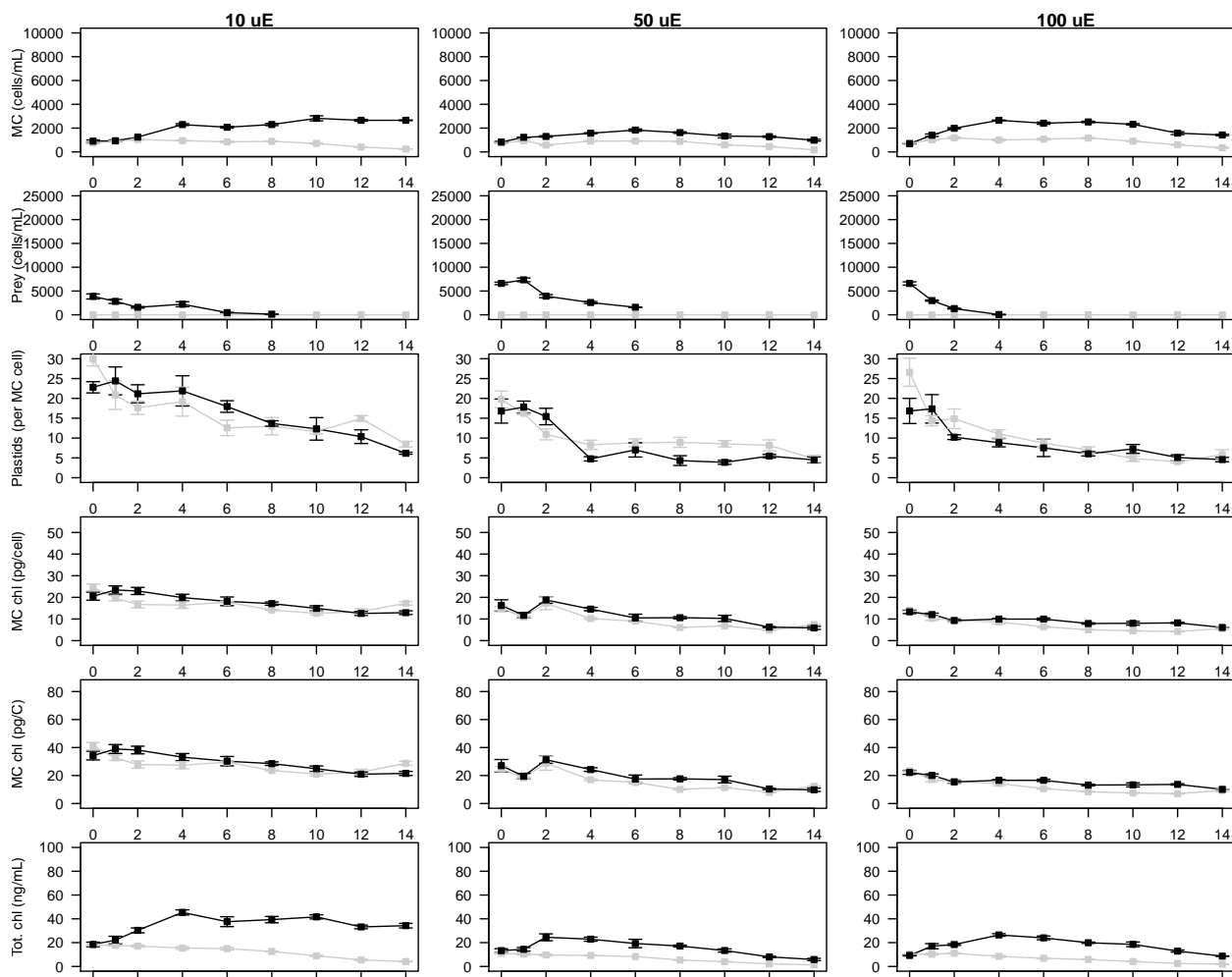
MC (cells/mL)

Prey (cells/mL)

Plastids (per MC cell)
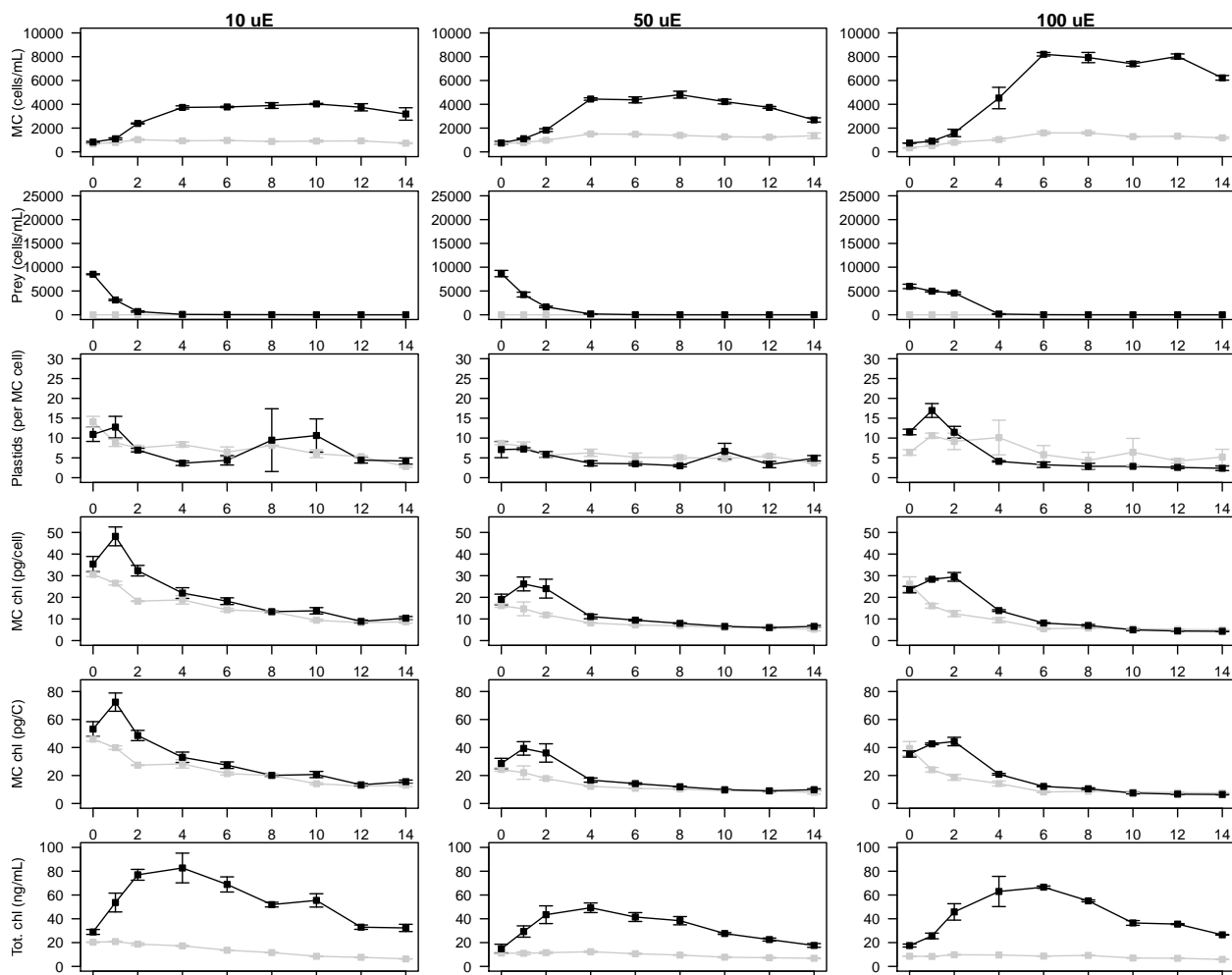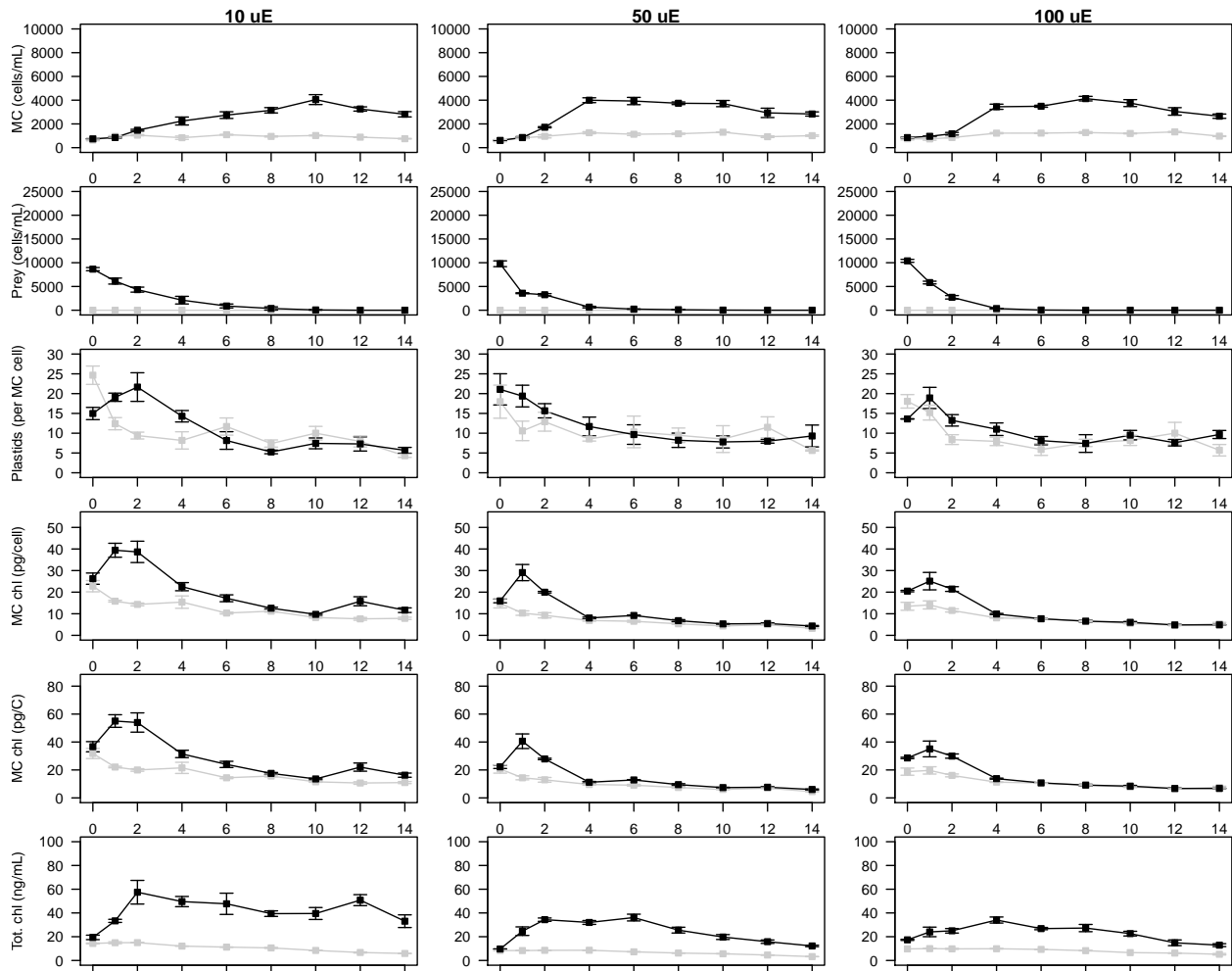
MC chl (pg/cell)

MC chl (pg/C)

Tot. chl (ng/mL)

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Supplementary Figures: Photophysiology timeseries

```r
# Choose the data columns to use, their names, and their maxima
datcols <- c(12,21,dim(dat)[2]-4,dim(dat)[2]-3) # data columns to use. CHECK THIS CAREFULLY
ylabstrs <- c('Photosynth. Eff. (Fv/Fm)','ETR','PI_chl','PI_cell') # y-labels
ymax <- rbind(rep(0.6,3),c(20,80,150),c(2,5,10),c(30,100,150))
ymin <- c(0.1,0,0,0)

# We will partition data by light level
lightvec <- c(10,50,100)
titlestr <- paste(as.character(lightvec),'uE'); titlestr <- rbind(titlestr,c(rep('',4)),c(rep('',4)),c(:

# Iterate over different prey types
preyvec <- c('CM','HP','RS','SM')

# Step 1: choose your prey type & subset data

for(k in 1:length(preyvec)){

# Step 1: Choose the prey and subset data accordingly
preychoice <- preyvec[k]
```

```r
dat.hold2 <- dat[dat$Prey==preychoice,]
crypto.hold2 <- crypto.dat[crypto.dat$Prey==preychoice,]


par(mar=c(2,4,2,1),mfcol=c(length(datcols),length(lightvec)))
# Note that we've used the argument "mfcol" instead of "mfrow." This ensures that the subsequent mega-p

for(j in 1:length(lightvec)){

# Step 2: Subset the data again for appropriate light level
dat.hold <- dat.hold2[dat.hold2$Light==lightvec[j],]
crypto.hold <-crypto.hold2[crypto.hold2$Light==lightvec[j],]
# Step 3: Create summary stats.
summ.FvFm<-summarySE(data=dat.hold,measurevar="FvFm",groupvars=c("ExptDay",'Fed'),na.rm=TRUE); crypto.Fv
summ.ETR <- summarySE(data=dat.hold,measurevar='ETR_I',groupvars=c("ExptDay",'Fed'),na.rm=TRUE); crypto

summ.PIchl<-summarySE(data=dat.hold,measurevar="PI_chl",groupvars=c("ExptDay",'Fed'),na.rm=TRUE); crypto
summ.PIcell<-summarySE(data=dat.hold,measurevar="PI_cell",groupvars=c("ExptDay",'Fed'),na.rm=TRUE); cry

# Step 4: Make all the plots
for(i in 1:length(datcols)){

# Create axes using raw data
plot(dat.hold$ExptDay, dat.hold[,datcols[i]], type='n', las=1, ylab=ylabstrs[i], xlab='', main=titlestr

if(i == 1){ summ.use <- summ.FvFm; crypto.use<-crypto.FvFm }; if(i == 2){ summ.use <- summ.ETR; crypto.u

# Plot lines connecting means
lines(summ.use[summ.use$Fed=='N',]$ExptDay,summ.use[summ.use$Fed=='N',][,4],col= Starvedcol); lines(summ

# Plot std error
summ.use.Y <- summ.use[summ.use$Fed=="Y",]; summ.use.N <- summ.use[summ.use$Fed=="N",]
arrows(summ.use.Y$ExptDay,summ.use.Y[,4]+summ.use.Y$se,summ.use.Y$ExptDay,summ.use.Y[,4]-summ.use.Y$se,

# Plot means
points(summ.use$ExptDay,summ.use[,4],pch=22,col=c(Starvedcol,Fedcol)[summ.use$Fed],bg=c(Starvedcol,Fedc

}}
}
```
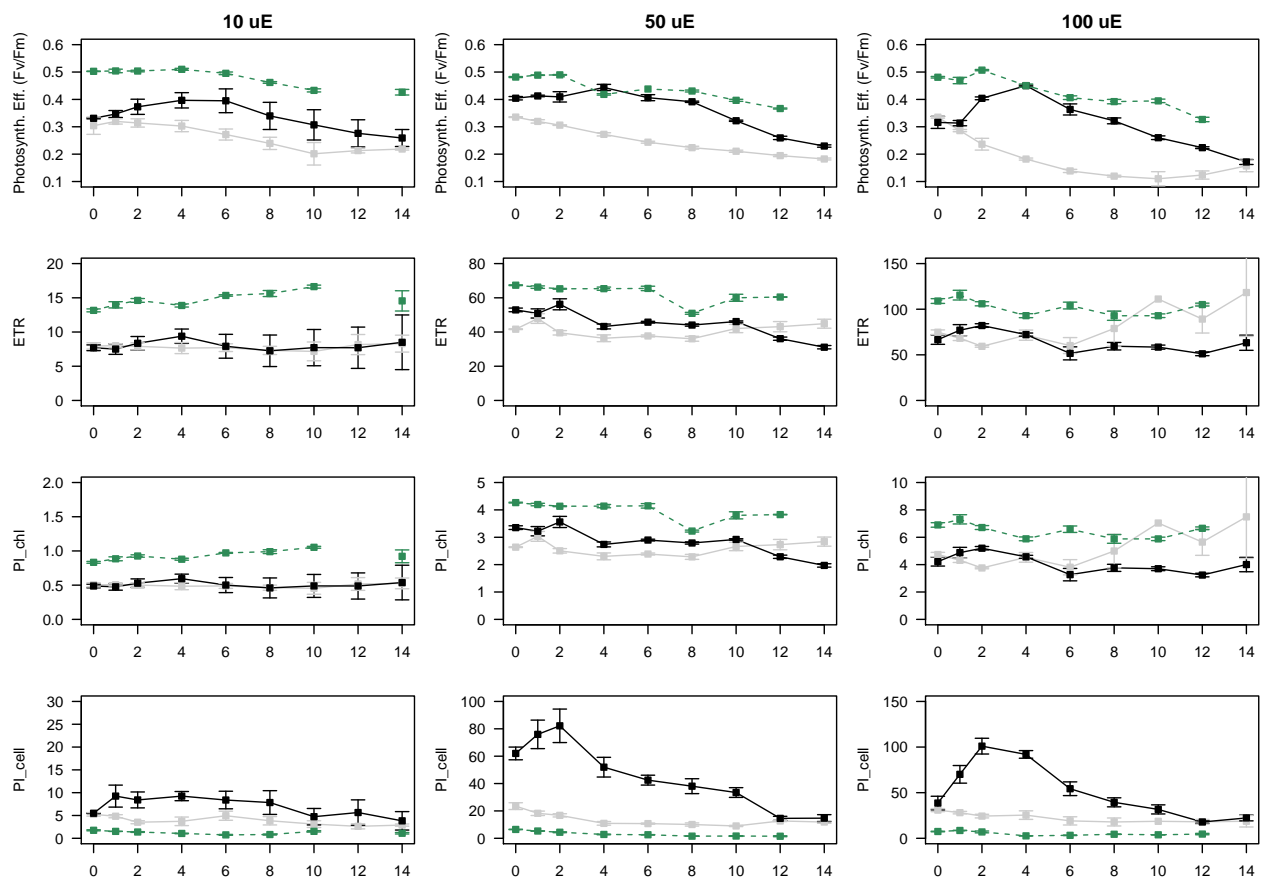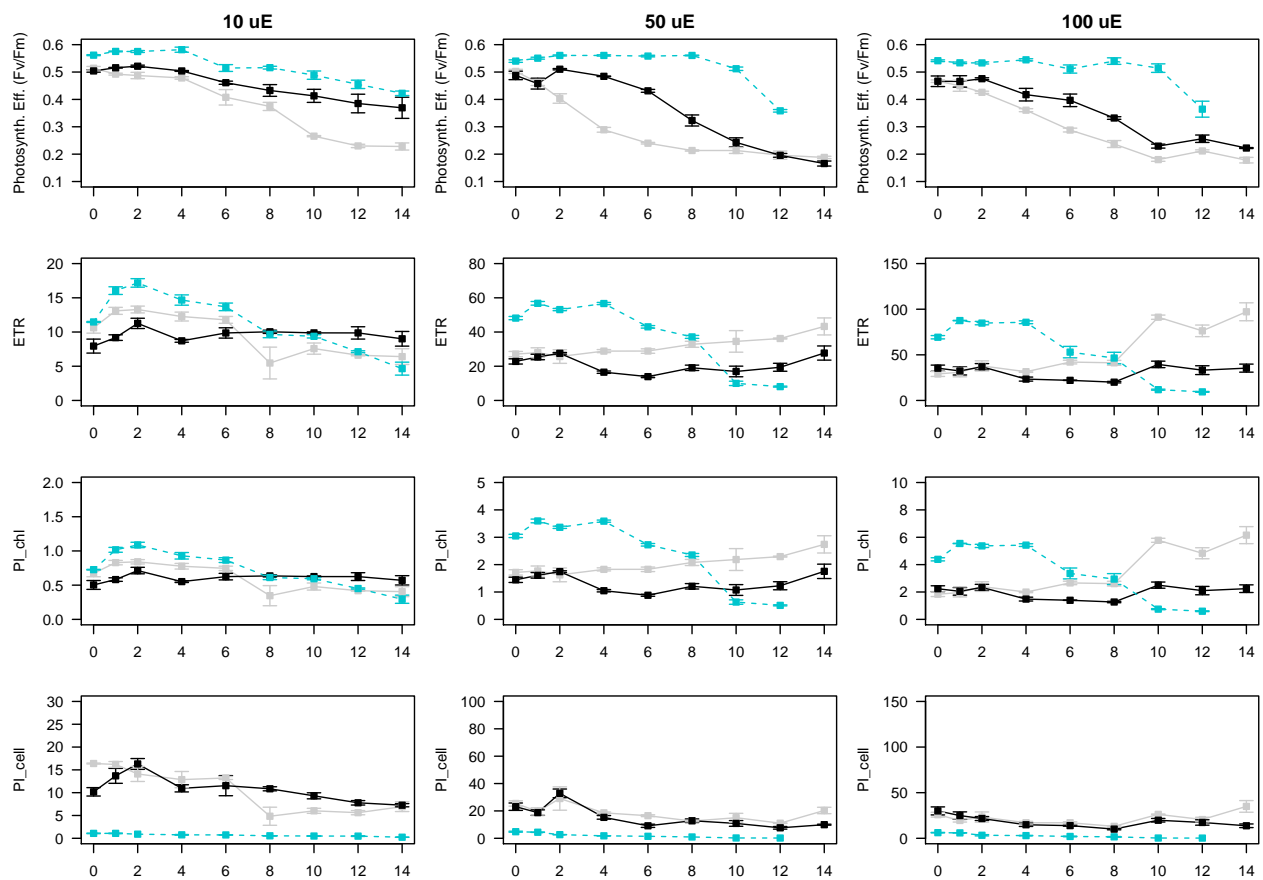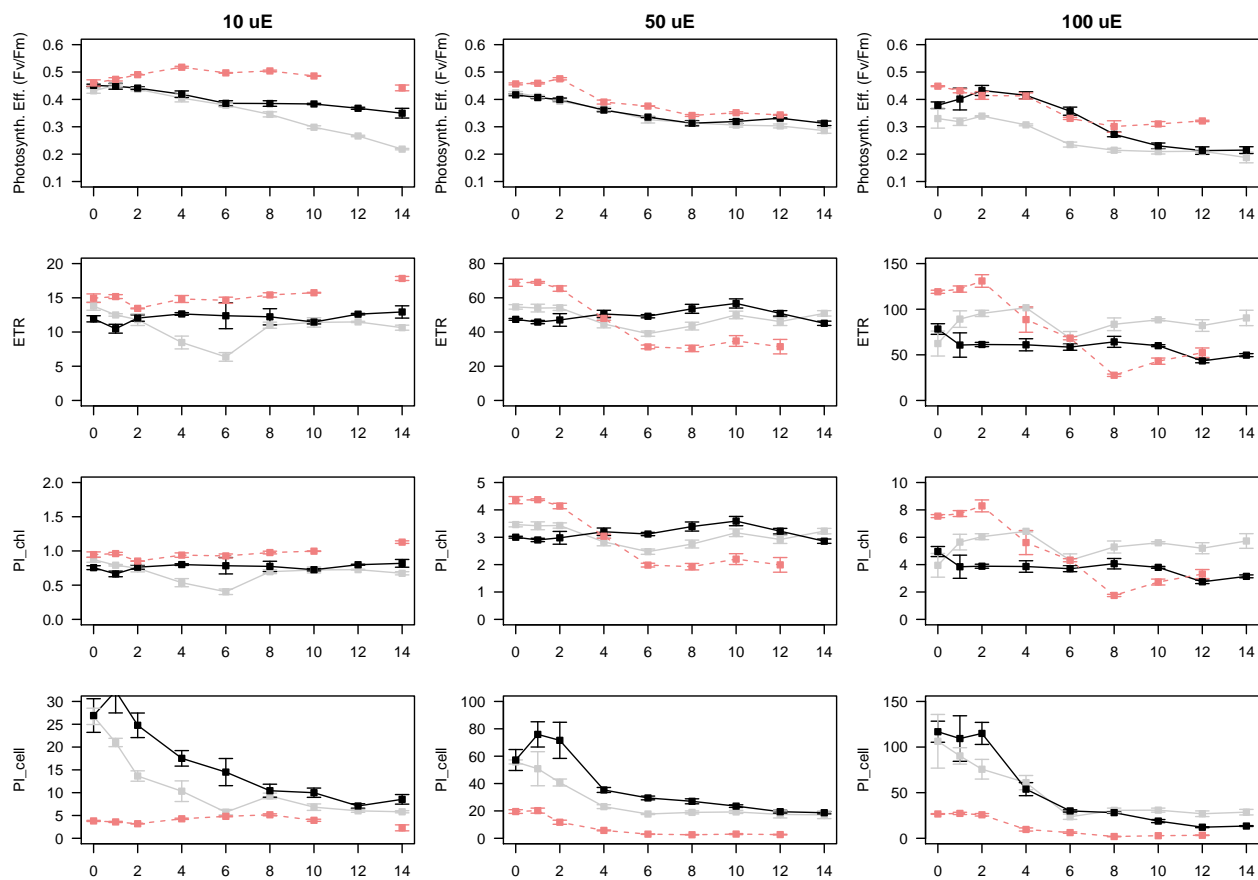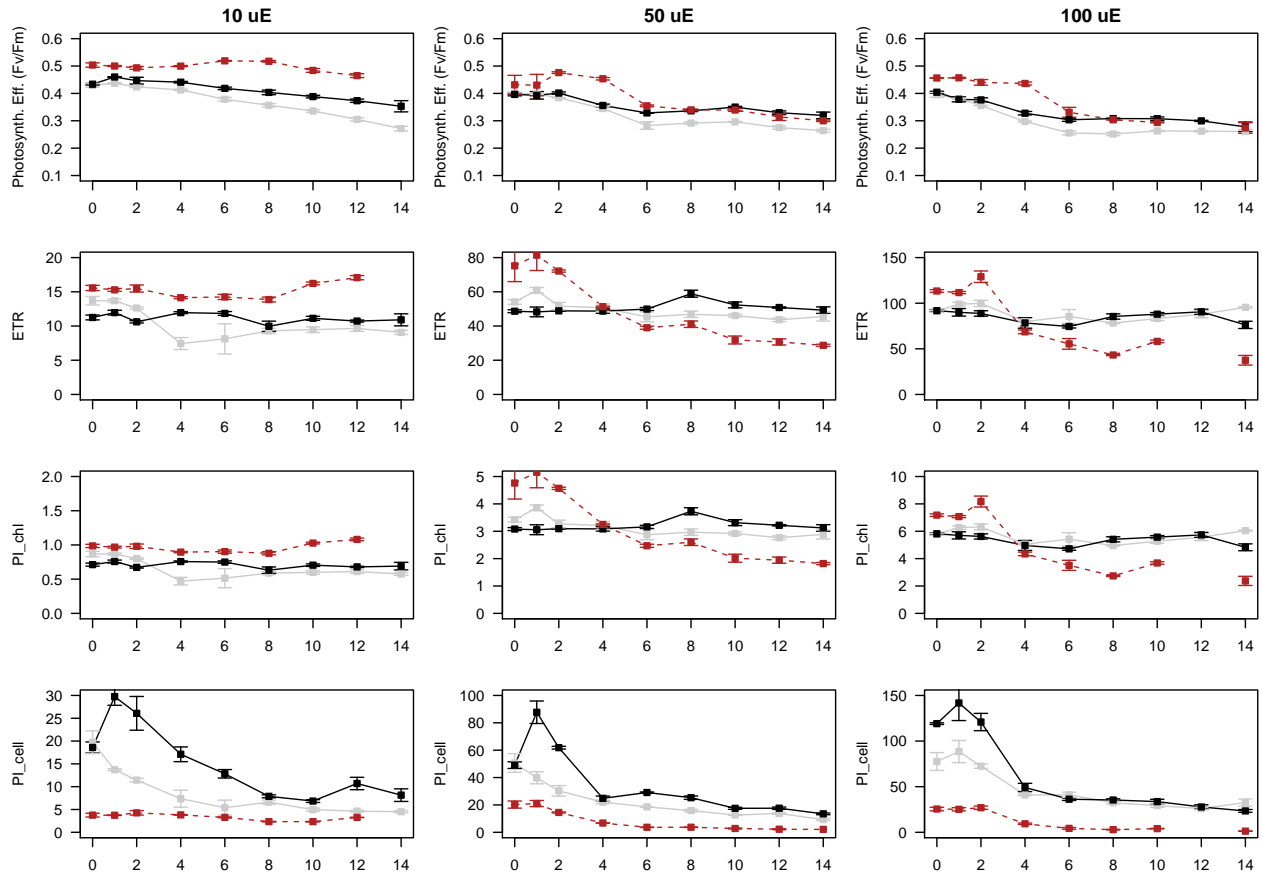
Supplementary Figures: Photophysiology timeseries, revision 1

```r
# Choose the data columns to use, their names, and their maxima
datcols <- c(which(names(dat)=='FvFm'),which(names(dat)=='a'),which(names(dat)=='Pmax'),which(names(dat)
ylabstrs <- c('Photosynth. Eff. (Fv/Fm)','alpha','Pmax','PI_chl','PI_C','PI_cell') # y-labels
ymax <- rbind(rep(0.6,3),c(2.3,3,3),c(150,200,250),c(2,5,10),c(100,400,500),c(35,100,160))
ymin <- c(0.1,0,0,0,0,0)

# We will partition data by light level
lightvec <- c(10,50,100)
titlestr <- paste(as.character(lightvec),'uE'); titlestr <- rbind(titlestr,c(rep('',3)),c(rep('',3)),c(

# Iterate over different prey types
preyvec <- c('CM','HP','RS','SM')

# Step 1: choose your prey type & subset data

for(k in 1:length(preyvec)){

# Step 1: Choose the prey and subset data accordingly
preychoice <- preyvec[k]
dat.hold2 <- dat[dat$Prey==preychoice,]
crypto.hold2 <- crypto.dat[crypto.dat$Prey==preychoice,]
```

```
par(mar=c(1,4,1,.1),mfcol=c(length(datcols),length(lightvec)))
# Note that we've used the argument "mfcol" instead of "mfrow." This ensures that the subsequent mega-p

for(j in 1:length(lightvec)){

# Step 2: Subset the data again for appropriate light level
dat.hold <- dat.hold2[dat.hold2$Light==lightvec[j],]
crypto.hold <-crypto.hold2[crypto.hold2$Light==lightvec[j],]
# Step 3: Create summary stats.
summ.FvFm<-summarySE(data=dat.hold,measurevar="FvFm",groupvars=c("ExptDay",'Fed'),na.rm=TRUE); crypto.F
summ.ETR <- summarySE(data=dat.hold,measurevar='PI_C',groupvars=c("ExptDay",'Fed'),na.rm=TRUE); crypto.

summ.alpha <- summarySE(data=dat.hold,measurevar='a',groupvars=c("ExptDay",'Fed'),na.rm=TRUE); crypto.a
summ.Pmax <- summarySE(data=dat.hold,measurevar='Pmax',groupvars=c("ExptDay",'Fed'),na.rm=TRUE);
if(preychoice=='CM'){if(j == 3){summ.Pmax[13,4]<-NaN}}
crypto.Pmax <- summarySE(data=crypto.hold,measurevar='Pmax',groupvars=c("ExptDay"),na.rm=TRUE); crypto.

summ.PIchl<-summarySE(data=dat.hold,measurevar="PI_chl",groupvars=c("ExptDay",'Fed'),na.rm=TRUE); crypto
summ.PIcell<-summarySE(data=dat.hold,measurevar="PI_cell",groupvars=c("ExptDay",'Fed'),na.rm=TRUE); cry

# Step 4: Make all the plots
for(i in 1:length(datcols)){

# Create axes using raw data
plot(dat.hold$ExptDay, dat.hold[,datcols[i]], type='n', las=1, xlab='', main=titlestr[i,j],ylim=c(ymin[

if(i == 1){ summ.use <- summ.FvFm; crypto.use<-crypto.FvFm }; if(i == 2){ summ.use <- summ.alpha; crypt

# Plot lines connecting means
lines(summ.use[summ.use$Fed=='N',]$ExptDay,summ.use[summ.use$Fed=='N',][,4],col= Starvedcol); lines(sum

# Plot std error
summ.use.Y <- summ.use[summ.use$Fed=="Y",]; summ.use.N <- summ.use[summ.use$Fed=="N",]
arrows(summ.use.Y$ExptDay,summ.use.Y[,4]+summ.use.Y$se,summ.use.Y$ExptDay,summ.use.Y[,4]-summ.use.Y$se,

# Plot means
points(summ.use$ExptDay,summ.use[,4],pch=22,col=c(Starvedcol,Fedcol)[summ.use$Fed],bg=c(Starvedcol,Fedc

}}
}
```